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April 1, 2004, 14:52:43 ; Search time 53.2407 Seconds (without alignments) 1302.928 Million cell updates/sec
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125
1 TIGGCCACTCCCTCTGCG.......CGCAGAGAGAGAGAGTGGCCAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents NA:*
1: /cgn2_6/ptodate/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodate/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodate/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodate/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodate/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodate/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                  682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

į	Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli	Appli Appli Appl Appl Appl Appli Appli Appli Appli Appli Appli
Description	Sequence 1, Applissequence 1, Applissequence 1, Applisequence 4, Applisequ	6611997788
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QI	US. 00 0 0 0 0 0 0 0	US-09-299-141-8 US-08-299-141-8 US-08-893-327-15 US-08-893-327-15 US-08-893-327-17 US-08-893-327-17 US-08-893-327-19 US-09-299-141-1 US-09-299-141-6 US-09-299-141-6
		446666664444
% Query Match Length DB	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6142 6142 6253 6280 6280 6280 6280 6280 6280
% Query Match		
Score	25 25 25 25 25 25 25 25 25 25 25 25 25 2	
Result No.	0 0 11111111111111111111111111111111111	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Sequence 9, Appli Sequence 10, Appli Sequence 10, Appl Sequence 11, Appl Sequence 11, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli		ength 145; Indels 0; Gaps 0; CGGGCGACCAAAGGTCGCC 60 CGGGCGACCAAAGGTCGCC 60	AGCGCGCAGAGAGGGAGTG 120
125 100.0 6924 4 US-09-299-141-9 125 100.0 6924 4 US-09-299-141-9 125 100.0 6924 4 US-09-299-141-10 125 100.0 6924 4 US-09-299-141-10 125 100.0 6924 4 US-09-299-141-10 125 100.0 6924 4 US-09-299-141-11 125 100.0 6924 4 US-09-299-141-11 125 100.0 6924 4 US-09-299-141-1 125 100.0 6924 4 US-09-299-141-7 125 100.0 7054 4 US-09-299-141-3 125 100.0 7054 4 US-09-299-141-3 125 100.0 7405 4 US-09-299-141-2 125 100.0 7405 4 US-09-299-141-5 127 100.0 7405 4 US-09-299-141-5 128 97.4 5585 2 US-08-304-110A-1	ALIGNMENTS 1-1 25249 CORMATION: SIVAGETURY, Arun INVENTION: SAFE VECTOR FOR GENE THERAPY SEQUENCES: ES: Scully, Scott, Murphy Presser 400 Garden City Plaza Garden City New York SCHIPL, SCOTT, Murphy Presser 400 Garden City Plaza Garden City New York SCHIPL, SCOTT, Murphy Presser 1530 SETTER COMPACTOR FOR GENE THERAPY SEQUENCES: ES SCULLY, SCOTT, Murphy Presser Garden City New York SCHIPL CAPPON GASK READABLE FORM: READABL	/ Match Local Similarity 100.0%; Score 125; DB 1; Length 145; Local Similarity 100.0%; Pred. No. 7e-25; Indels 0; Gaps Les 125; Conservative 0; Mismatches 0; Indels 0; Gaps Traccorrecterrecognesses of Indels 0; Gaps 1 Traccorrecterrecognesses of Indels 0; Gaps	. 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-07-789- Sequence Parent Name CORRE C	Query Ma Best Loc Matches Qy Db	ì &

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US-07-982-193-1
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LATTA, Martine
APPLICANT: LATTA, Martine
APPLICANT: DENEFLE, Patrice
APPLICANT: DENEFLE, Patrice
APPLICANT: VIGUE, Emmanuelle
APPLICANT: VIGUE, Emmanuelle
APPLICANT: VIGUE, Emmanuelle
APPLICANT: VIGUE, Mananuelle
APPLICANT: VIGUE, Mananuelle
TITLE OF INVENTION: INTEGRATIVE RECOMBINANT ADENOVIRUSES,
TITLE OF INVENTION: PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poullenc Rorer Inc.
STREET: 500 Arcola Rd, 3C43
CITY: Collegeville
STREET: VA
COUNTRY: USA
ZIP: 19426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TIGGCCACTCCCTCTCTGCGCGCCTCGCTCACTGAGGCCGGGCGAACGTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc_feature
) LOCATION: 1..145
) OTHER INFORMATION: /note= "Minimal ITR Sequence"
US-08-702-573-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING WATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/02445
FILING DATE: 03-MAR-1994
PRIOR APPLICATION NUMBER: WO PCT/FR95/00233
APPLICATION NUMBER: WO PCT/FR95/00233
FILING DATE: 28-FEB-1995
ATTORNEY/AGENT INNORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST94011-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08702573 Patent No. 6033885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 125, Conservative
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125 TTGGCCACTCCCTCTCTGCGCTCGCTCGCTCACTGAGGCCGGGCGAAGGTCGCC
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                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: NATSOULIS, GEORGES
APPLICANT: NATSOULIS, GEORGES
APPLICANT: REMOSKY, RICHARO TITLE OF INVENTION: TARGETED NUCLECTIDE SEQUENCE DELIVERY
TITLE OF INVENTION: TARGETED NUCLECTIDE SEQUENCE
INVENTES OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STATE: CA
COUNTRY: USA
COMPUTRY: Palo Alto
STATE: CA
COMPUTRY: IBM PC COMPATIBLE
COMPUTER: PREPABLE FORM:
COMPUTER: PREPABLE FORM:
COMPUTER: BENEUT NELSES: #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,866
FILING DATE: 08-SEP-1995
CLASSIFICATION STATE: 08-SEP-1995
CLASSIFICATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 0800-0006
TELECOMMUNICATION INFORMATION:
NAME: ROBINS, ROBERTA L.
RECASIFICATION NUMBER: 037-323
INFORMATION POR SEQ ID NO: 1:
RECASIFICATION NUMBER: 0800-0006
TELEPAX: (415) 327-3231
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs
TYPE: INCIDIAL SCIENCE
TYPES THAT SCIENCE
TYPES
TY
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Patent No. 6261834
GENERAL INFORMATION:
APPLICANT: Stivastava, Arun
TITLE OF INVENTION:
SAFE VECTOR FOR GENE THERAPY
CORRESPONDENCE ADDRESS:
2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                              US-08-525-866-1/c
; Sequence 1, Application US/08525866
; Patent No. 6207457
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121 GCCAA 125
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Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0; Indele (
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Sequence 7.8A-1
Patent No. 5869305
GENERAL INFORMATION:
APPLICANT: Xiao, X.
TITLE OF INVENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COMPUTR: New York
COMPUTR: New York
COMPUTR: New York
COMPUTR: BAP COMPATIBLE
COMPUTR: BAP COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,738A
FILING DATE: Patentin Release #1.0,
NAME: COLUZZ, LAURA #35
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, LAURA #35
ATTORNEY/AGENT INFORMATION:
TELECOMUNICATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6636-022
TELECOMUNICATION INFORMATION:
TELECO
                                                   ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LGUTA A
REGISTATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 6636-013
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEX: 66141 PENNE
INFORWATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 bace pairs
TYPE: mucleic acid
STRANBEDNES: double
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MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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100.0%; Score 125; DB 3; Length 1.
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07989841A
Sequence 1, Application US/07989841A
Patent No. 5478745
GENERAL INFORMATION:
APPLICANT: Xiao, X.
TITLE OF INVENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-271.
ZIP: 10036-271.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM C compatible
COMPUTER: IS
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER IEBAPC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 19921125
CLASSITCATION NUMBER: US/07/982,193
FLING DATE: 19921125
ATTORNEY/AGENT INFORMATION:
NAME: MANLI WILLIAM E.
REGISTRATION NUMBER: 22,606
REGISTRATION NUMBER: 22,606
REGISTRATION NUMBER: 23,606
REGISTRATION SANS US
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4366
TELEPAX: (516) 742-4366
TELEPAX: C16) 742-
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear _
MOLECULE TYPE: DNA (genomic)
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US-07-989-841A-1
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TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE:
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                                                                                                                                             1 TIGGCCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGGGGACCAAAGGTCGCC
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                                                                      Query Match 100.0%; Score 125; DB 2; Length 165; Best Local Similarity 100.0%; Pred. No. 7e-25; Matches 125; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08471914A
; Patent No. 6057152
; GENERAL INFORMATION:
; APPLICANT: SamulbKi, R.
; APPLICANT: SamulbKi, R.
; TITIE OF INVENTION: RECOMBINANT VIRAL VECTOR SYSTEM
; FILE REPERENCE: 6636-027
; CURRENT APPLICATION NUMBER: US/08/471,914A
; CURRENT FILING DATE: 1995-06-06
; EARLIER PILING DATE: 1995-05-15
; NUMBER OF SEQ ID NOS: 13
; SOFFWARE: Patentin Ver. 2.0
; SEQ ID NO :
; LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7. Application US/09276625
Patent No. 6436392
GENERAL INFORMATION:
APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: A5.007US1
CURRENT APPLICATION NUMBER: US/09/276,625
CURRENT FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

100.0%; Score 125; DB 3;
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0;
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-440-738A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                        GCCAA 125
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US-09-276-625-7
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                                                                                              1 TTGGCCACTCCCTCTCTGCGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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             Indels
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/M3-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,391
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,358
FILING DATE:
APPLICATION NUMBER: 35,302
REGISTRATION: WUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 125; DB 1;
ilarity 100.0%; Pred. No. 7.9e-25;
Conservative 0; Mismatches 0;
             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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STRANDENESS: Sira
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
             Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 125; Conserv
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US-08-475-391-1
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Patent No. 5658785

GENERAL INPORMATION:

TITLE OF INVENTION: Adeno-Associated Virus Materials and TITLE OF INVENTION: Methods

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES: ACORESES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 111,nois

COUNTRY: USA

ZIP: 60606

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/254,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125; DB 1; Length 4680; Pred. No. 7.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FRATURE:
NAME/KEY: misc_feature
LOCATION: 1..192
OTHER INFORMATION: /note= "Right ITR Sequence in patent No. 6033885
US-08-702-573-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 125; DB 3;
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658785and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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; MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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TYPE: DNA

CRCANISM: Artificial Sequence

PRATURE:

CHERINE NFORMATION: Description of Artificial Sequence:p43C-AT

US-09-181-4
                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPAGE
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07178
FILING DATE:
CLASSIFICATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LYPE: NUCLEIC acid
TYPE: NUCLEIC ACID
                    6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: DNA (genomic) PCT-US95-07178-1
STREET: 65.
CITY: Chicago
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                                                                 STATE: I
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US-09-299-141-4
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Sequence 1, Application US/08709609

Patent No. 5858775

GENERAL INPORMATION:

APPLICANT: Johnson, Philip R.

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCE: 3

CORRESPONDENCE ADDRESS:

ADDRESSES:

ADDRESSES:

ADDRESSES:

ADDRESSES:

ADDRESSES:

ADDRESSES:

ADDRESSES:

COUNTRY: USA

COUNTRY: USA

ZIP: 6606

COUNTRY: USA

ZIP: 6606

COMPUTER READALLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4680;
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TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.9e-25;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: NO. 5858775and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9507178; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-709-609-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAA 125
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                           121 GCCAA 125
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Query Match
100.0%; Score 125; DB 5; Length 4680;
Best Local Similarity 100.0%; Pred. No. 7.9e-25;
Matches 125; Conservative 0; Mismatches 0; Indels 0
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Sequence 4, Application US/09299141

Patent No. 6461606

GENERAL INFORMATION:

APPLICANT: FLOTTE, TERRICE R.

APPLICANT: SONG, SIHONG

APPLICANT: MORGAN.

TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY

TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY

FILE REPERENCE: 4300.011800

CURRENT APPLICATION NUMBER: US/09/299,141

CURRENT PILING DATE: 1999-04-23

SERLIER APPLICATION NUMBER: 60/083,025

EARLIER PILING DATE: 1998-04-24

SEQ ID NO 4

SEQ ID NO 4

LENGHH: 5932

TUBER 1832
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Query Match
Best Local Similarity 100.0%; Pred. No. 8e-25;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps
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US-09-141-4/c
US-09-141-4/c
Sequence 4, Application US/09299141
Fatent No. 6451606
FABURALI INFORMATION:
APPLICANT: FLOTTE, TERENCE R.
APPLICANT: SONG, SIRONG
FILE REFERENCE: 4300.011800
CURRENT APPLICATION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REFERENCE: 4300.011800
CURRENT APPLICATION NUMBER: US/09/299,141
FILE REPERENCE: 1300.011800
CURRENT PILING DATE: 1999-04-23
EARLIER PILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTING DATE: 1998-04-24
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 5932
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100.0%; Score 125; DB 4; Length 5932;
Best Local Similarity 100.0%; Pred. No. 8e-25;
Matches 125; Conservative 0; Mismatches 0; Indels 0.
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:p43C-AT
US-09-299-141-4
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	
on: April 1, 2004, 14:05:53 ; Search time 1573. (without alignmen 3442.959 Million	1573.61 Seconds gnments) lion cell updates/sec
Title: Perfect score: 125 Sequence: 1 TIGGCCACTCTCTCTGCGCGCAGAGAGGACA	.CGCAGAGGGAGTGGCCAA 125
Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched: 3470272 segs, 21671516995 residues	
Total number of hits satisfying chosen parameters: 69405	6940544
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl: * 1: gb ba: * 2: gb_hcg: * 4: gb_on: * 5: gb_ov: * 6: gb_pt: * 10: gb_pt: * 10: gb_pt: * 11: gb_bv: * 11: gb_bv: * 11: gb_pv: * 11: gb_vv: * 12: gb_pv: * 13: gb_vv: * 14: gb_vv: * 15: em_bv: * 16: em_fun: * 17: em_fun: * 18: em_fun: * 19: em_mv: * 21: em_ov: * 22: em_ov: * 22: em_ov: * 23: em_pt: * 24: em_pt: * 25: em_pv: * 25: em_pv: * 26: em_pv: * 27: em_pv: * 28: em_hcg_hum: * 30: em_hcg_hum: * 31: em_hcg_ohum: * 33: em_hcg_ohum: * 34: em_hcg_ohum: * 35: em_hcg_ohum: * 36: em_hcg_ohum: * 37: em_hcg_ohum: * 38: em_hcg_ohum: * 38: em_hcg_ohum: * 39: em_hcg_ohum: *	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		AX38 A464	AR140333 Sequence	AX286293 Sequence	KO1	M10681 Adeno-ass	ARO3	AR22	AX10	BD21	A464	AX70349	301	AX13580	AX28629	BD09455	J01901	AX28248	AF02	1623	BD24	BD24	AR235457 Sequenc	AR23	AR23	AR23	AK23 AR23	AR23	AR23	AKZ3	AR23	AR23	AR23	ARZ3	ARZ3	AR235456 AR235456 Sequence	ALIGNMENTS		130 bp DNA linear PAT 19-MAR-2002 WO0214526.		0.	2.2	; Farvoviridae; Farvovirinae; Dependovirus;	aav helper functions . 21-FBB-2002;
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FEATURES

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Adeno-associated virus 2
Adeno-associated virus 2
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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Unclassified.
1 (bases 1 to 145)
Natsoulis,G. and Surosky,R.T.
Targeted nucleotide sequence delivery and integration system
Targeted, 127-7-7-7 1 27-7-7-7 1 27-7-7-7 1 27-7-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-7 1 27-
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/organism="Adeno-associated virus 2"
/molltype="unassigned DNA"
db_xref="taxon:10804"
/note="ITR"
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Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 125; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                            /organism="unknown"
/mol_type="unassigned DNA"
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Cytotoxic agents
Patent: WO 0180840-A 2 01-NOV-2001;
BTG INTERNATIONAL LIMITED (GB)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX286293 145 bp
Sequence 2 from Patent WO0180840.
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1 (bases I to 145)
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1 INTEGRATIVE RECOMBINANT ADENOVIRUSES, PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
PATCHIC WO 95238677A 4 08-SEP-1995;
RHONE POULENC ROKER SA (FR)
Other publication AU 1852695 950918
Other publication AU 1852695 950908.
Location/Qualifiers
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100.0%; Score 125; DB 6; Length 1:
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 125; Conservative 0; Mismatches 0; Indels
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    forganism="Adeno-associated virus 2"
/mol type="unassigned DNA"
    /db_xref="taxon:10804"

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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 1 from patent US 6207457.
AR140333 GI:14482829
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Sequence 4 from Patent WO9523867
A46401
   Location/Qualifiers
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Adeno-associated virus 2H
Adeno-associated virus 2H
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Lusby, E., Fife, K. H. and Berns, K. I.
Nucleotide sequence of the inverted terminal repetition in adeno-associated virus DNA
J. Virol. 34 (2), 402-409 (1980)
80185149
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Lefebvre, R.B., Riva, S. and Berns, K.I.
Conformation takes precedence over sequence in adeno-associated
virus DNA replication
Mol. Cell. Biol. 4 (7), 1416-1419 (1994)
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100.0%; Score 125; DB 14; Length 145;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 125; Conservative 0; Mismatches 0; Indels 0.
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replication; terminal repeat.
1 of 2
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RESULT 6 AA2LTR2

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Original Source text: Adeno-associated virus 2H DNA (clone pSM620 [2]), from KB or HeLa cells.

The focus of both papers is the method of replication of the virus. The focus of both papers is the method of replication of the time; it is shortened to tin 50% of the population and missing altogether is shortened to tin 50% of the population and missing altogether in 15% of the population. There is further sequence heterogeneity which cam be explained by assuming that the terminal 125 bases, which form an imperfect pallindrome, are replaced by their inverted complement during replication. [2] found that deletion of the 9 complement during replication. [2] found that deletion of the 9 cerminal bases on the right and the 11st terminal bases on the left of AAV 2 genome did not stop DNA replication. Further deletion of an 11-base symmetrical sequence (bases 89 to 99) in the right terminal repetition inhibits DNA replication. Substitution of either an 8-base (cagatots) or 12-base (cagatots) symmetrical sequence unrelated to the original 11-base sequence restores DNA replication. All of this can be explained by assuming that the 125 base palindrome mentioned above form a t-shaped secondary structure which provides a primer for DNA polymerase during replication.
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Adeno-associated virus 2H
Luses; SDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Lusby,E., Fife,K.H. and Berns,K.I.
Nucleotide sequence of the inverted terminal repetition in adeno-associated virus DNA
1, Virol. 34 (2), 402-409 (1980)
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Lefebruce, R.B., Riva, S. and Berns, K.I.
Conformation takes precedence over sequence in adeno-associated virus DNA replication
Mol. Cell. Biol. 4 (7), 1416-1419 (1984)
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AA2LTR2
Adeno-associated virus 2 right terminal sequence.
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'mol type="genomic DNA"
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/db_xref="taxon:10805"
22 bases upstream of HaeIII sites.
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 125; Conservative 0; Mismatches 0; Indels
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Samulski,R.J. and Xiao,X.
Recombinant viral vector system
Patent: US 5478745-A 1 26-DEC-1995;
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Engelhardt, 7.F. and Duan, D.
Adeno-associated virus vectors
Patent: US 6436392-A 7 20-AUG-2002;
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Sequence 7 from patent US 6436392.
AR223306
AR223306.1 GI:23331457
 Sequence 1 from patent US 5478745.
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                           GI:1251714
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     Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus. 1 (bases 1 to 145)
Berns, K.I., Hauswirth, W.W., Fife, K.H. and Lusby, E. Adeno-associated virus DNA replication Cold Spring Harb. Symp. Quant. Biol. 43 Pt 2, 781-787 (1979) 80023388
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/organis="Adeno-associated virus 2H"
/mol type="genomic DNA"
/db_xref="taxon:10805"

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Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 125; Conservative 0; Mismatches 0;
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Samulski, R. Jude, and Xiao, X.
Recombinant viral vector system
Patent: US 5869305-A 1 09-FEB-1999;
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Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 125; Conservative 0; Mismatches 0;
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Denefle, P., Latta, M., Perricaudet, M. and Vigne, E.
INTEGRATIVE RECOMBINANT ADENOVIRUSES, PREPARATION THEREOF AND
THERAPEUTICAL USES THEREOF
PATENT: WO 9523867-A 3 08-SEP-1995;
RHONE POULENC RORER SA (FR)
Other publication AU 1862695 950918
Other publication FR 2716893 950908.
Location/Qualifiers
                                100.0%; Score 125; DB 6; Length 1
100.0%; Pred. No. 2.7e-18;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 125; Conservative 0; Mismatches 0;
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 1 from Patent WO0192551.
AX418199 GI:21523203
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Sequence 3 from Patent WO9523867.
A46400.
A46400.1 GI:2300601
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          PAT 30-APR-2001
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28-MAY-2002
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20-MAY-1999 US 09/276625 PI
F ENGREMBARDT, DONGSHENG DUAN, TUYIN YANG
C12N1S/00, A01K67/027, A61K31/711, A61K48/00, C07K14/47, C12NS/10, C12N1S/00)
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Adeno-associated viruses and uses thereof
Patent: WO 0125465-A 7 12-APR-2001;
University of Iowa Research Foundation (US) ; Engelhardt, John F.
(US) ; Dongsheng, Duan (US) ; Ziying, Yan (US)
Location/Qualifiers
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Sequence 7 from Patent WO0125465.
AX106702
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JP 2002515257-A/7.
                                                                                                        AX106702.1 GI:13922363
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UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL (US)
Location/Qualifiers
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/db_Xref="taxon:32630"
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1. .207
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Anote="synthetic enzyme attachment site sequence"
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Best Local Similarity 100.0%; Pred. No. 2.6e-18;

Matches 125; Conservative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 2.6e-18;
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Procaryctic libraries and uses
Patent: WO 02066653-A 58 29-AUG-2002;
Xencor (US)
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Sequence 58 from Patent WO02066653.
AX703496.1 GI:29538456
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Scoring table:

Searched:

Minimum DB seq Maximum DB seq

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Secale cereale
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Epermaryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Secale.

I (bases 1 to 304)
Straderson,O.D., Han,P.S., Hsia,C.C., Kang,Y.,
Enton,R.D., Gustafon,J.P., Han,P.S., Hsia,C.C., Kang,Y.,
Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and
Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Anther obna library from rye
Upublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: $10559573
Fax: 5105595818
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BZ569259 pacs2-164
AG185368 Pan trog1
BY752719 BY752719
                                                                                                                                   April 1, 2004, 14:50:59 ; Search time 1603.24 Seconds (without alignments) 2328.267 Million cell updates/sec
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125
1 TIGGCCACTCCCTCTCTGCG.......CGCAGAGAGAGAGTGGCCAA 125
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1015)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M.,
Burns, J. L., Kaul, R. and Oleen, M. V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene Sk primer,
Location/Qualifiers
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 20622169544
Email: craymond@u.washington.edu
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aeruginosa'

/organism="Pseudomonas /mol_type="genomic DNA" /strain="2-164" /db_xref="taxon:287"

Class: shotgun. Location/Qualifiers

1. .1015

source

FEATURES

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"" (bases 1 to 1049)

"E ' (bases 1 to 1049)

"E Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

"Totoki, Y., Watanabe, H. and Sakaki, Y.

"Interpretable to English and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

"Interpretable to Chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesgec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.81-45-503-9111, Fax:81-45-503-9170)

"Tones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes DNA, clone: RP43-059G23.TJ, genomic survey sequence. AG185368 AG185368 ... GISTONESSES AG185368 ... GISTONESSES AG185368. GISTONESSES AG185368. Pan troglodytes (chimpanzee) Plan troglodytes (chimpanzee) Plan troglodytes
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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/clone="pacs2-164_8319"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library.
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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BAC end sequences of Library RPCI-43
Unpublished
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                                                                                                                                                                                   Indels
                                                                                                                                    ch 29.9%; Score 37.4; DB 28; 1 Similarity 56.7%; Pred. No. 61; 68; Conservative 0; Mismatches 52;
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/organism="Pan troglodytes"
/mol_type="denomic DNA"
/db xref="taxon:9598"
/clone="RP43-059G23.TJ"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Matches 68; Conserv
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Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 644)

Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kayosawa, H.; Yagai, K.; Tomaru, Y.; Hasegawa, Y.; Mogami, A.; Kayosawa, H.; Yagai, K.; Tomaru, Y.; Hasegawa, Y.; Mogami, A.; Schonbach, C.; Gojobori, T.; Baldarelli, R.; Hilli, D.; Bult, C.; Grobani, L. E.; Cousine, S.; Dalla, E.; Brusic, Y.; Chothia, C.; Corbani, L. E.; Cousine, S.; Dalla, E.; Dragani, T. A.; Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gaasterland, T.; Gustinocich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E.D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R.N.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Lee, Y.; Lenhard, B.; Lomis, P.; Maltais, L.; Marchhonni, L.; McKenzie, L.; Mish, H.; Magashima, T.; Navasi, T.; Reed, J. C.; Reed, D. J.; Reing, P.; Ranchandran, S.; Ravasi, T.; Reed, J. C.; Red, D.J.; Rig, B. E.; Ringwald, M.; Sandellin, A.; Schneider, C.; Semple, C.A.; Setou, M.; Shimada, K.; Sandai, T.; Reed, J. C.; Wang, Y.; Maranabe, Y.; Wanger, L.; Wanger, L.; Wanger, L.; Wanser, M.; Yang, I.; Wanger, L.; Wanser, M.; Yang, I.; Yang, I.; Yang, I.; Yang, I.; Wanger, L.; Wanser, M.; Yang, I.; Yang, I.; Yang, I.; Wanger, L.; Wanser, M.; Yang, I.; Yang, I.; Wanger, L.; Wanser, M.; Yang, I.; Wanger, I.; Wangawa, T.; Rukud, S.; Hara, A.; Hashizume, M.; Yang, I.; Cho, Wangawa, T.; Rukud, S.; Hara, A.; Hashizume, W.; Waterston, R.; Lander, M.; Rasawa, T.; Rukud, S.; Hara, A.; Hashizume, W.; Waterston, R.; Arakawa, T.; Rukud, S.; Hara, A.; Hara, A.; Yasunishi, A.; Sasaki, W.; Sasaki, D.; Sasaki, S.; And Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cubms
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-92
Fax: 81-45-50
                                                                                                                                                                                                                                                                        644 bp mRNA linear EST 17-DEC-2002 BY752719 RIKEN full-length enriched, adult inner ear Mus musculus EDNA clone F930013F16 5', mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
121
                                                                                      467 CGCCCGCCCGGGGGGGGGGGTCTCGCCGTGCCGGGGGCCGGCGCTCCCGGGGTGG 410
Contact: Yoshihide Hayashizaki
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genome Cstences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://willlength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH12FF1.
Location/Qualifiers
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/clone_lib="RIKEN full-length enriched, adult inner ear"
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    .644
    /organism="Mus musculus"
/mol type="mRNA"
    /strain="C57BL/6J"

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/db_xref="taxon:9606"
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tissue_type="inner ear"
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18 GCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGC
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1 Similarity 56.5%;
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone=lib="NHH_MGC_41"
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Buperseript II RT (Life Technologies). Note: this is a
NHH_MGC Library."
                 /tissue type="PLACENTA"

/close Tib="Homo sapiens PLACENTA"

/close Tib="Homo sapiens PLACENTA"

/note="Woctor: pMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer of the prime end cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENCOURT 6581988 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5472226
57, mENA Sequence.
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                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (Dases 1 to 1182)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1981 row: o column: 11
High quality sequence stop: 290.
Location/Qualifiers
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                                                                                                                                                                                                     ch 28.3%; Score 35.4; DB 13; Similarity 11.7%; Pred. No. 1.9e+02; 13; Conservative 68; Mismatches 30;
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clone="CL0BA007ZH12"
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Best Local Similarity
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Indels

1. Similarity 57.1%; Pred. No. 1.9e+02; 50; Conservative 0; Mismatches 45;

Query Match Best Local Simi Matches 60;

Length 1182;

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/dev stage="adult"
/dev stage="adult"
/lab_host="adult"
/lab_host="adult"
/lab_host="lab":1006 - RescueMu Grid G" (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
dessigned to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site, 'www.randb.iastate-edu' and follow the links for
/RescueMu, 'Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on IB plates with
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1006082E08.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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Unpublished (2001)
Contact: Walbot V
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Zea mays
Lea mays
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
Plate: 1006082 row: 32
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Pred. No. 2e+02;
0; Mismatches 50; Indels
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_type="mixed background W23/A188/B73"
/db_type="leaf"
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/db_xref="taxon:10090"
/clone="InAGE:613467"
/lab_host="DHIWGE:613467"
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/clone_lorgan: otocysts; Vector: pCWV-SPORT6.1; Site_1:
EcoRV; Site_2: Not!, Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.95 kb. Constructed by
ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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BX403554 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA007ZH12
3-PRIME, mRNA sequence.
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                                                         896 bp mRNA linear EST 03-SEP-2002
8749018 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6334507
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                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I Chases 1 to 896)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llhl.gov.g column: 20

High quality sequence start: 3

High quality sequence stop: 683.
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Pred. No. 2.2e+02;
); Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th 28.0%; Score 35; DB Similarity 55.3%; Pred. No. 2.2e 68; Conservative 0; Mismatches
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                                                                                                                                                                   Mus musculus (house mouse)
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                                                                                         mRNA sequence.
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                                                                                               5', mRNA
BU152072
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I (Dases I to 530)
S Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-2299
Fax: 515-294-2299
Email: schnable@lastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/doorganism="Cideaooyzaiz"
/tissue type="FLACENTA"
/tissue type="FLACENTA"
/tissue type="FLACENTA"
/tissue type="FLACENTA"
/tissue type="FLACENTA"
/note="Worder: ponvSPGRT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECRNV sites of the pCWVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 14-NOV-2001
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E 1 (bases 1 to 1103)
S. Liw. B., Caubar.C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
L Unpublished (2001)
Contact: Genescope
Contact: Genescope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Email: seqrefégenoscope.ors.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Initrogen. Contact: Reng Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA007ZH12FP1.

Location/Qualifiers
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MEST88-F06.T3 ISUM4-TN Zea mays CDNA clone MEST88-F06 3', mRNA
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/clone="IGSODIO65YPO8"
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/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/once="Igt strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Best Local Similarity 28.9
Matches 35; Conservative
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BX338963.1 GI:30347036
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1 (bases 1 to 514)

1 (Jam. B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Brigi glu06 EVRY cedex - France
Email: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO65DH04QPI.
Location/Qualifiers
     as spacers.

PORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA FORWARD: Forward PCR primer sequence, primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.8%; Score 34.8; DB 12; Length 530;
larity 55.9%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                   tissue type="Seedling and silk"
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                                                                                                                                                                                                               /db xref="taxon:4577"
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Best Local Similarity
Matches 66; Conserv
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CG2BB16TH ZM 0.7 1.5 KB Zea mays genomic clone ZMWEMa0750D08, genomic survey sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.

I (bases I to Sus;
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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27.7%; Score 34.6; DB 13; Length 514; 28.9%; Pred. No. 2.4e+02; ive 43; Mismatches 43; Indels 0.
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Fax: 301-838-0208
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Class: sheared ends.
Location/Qualifiers
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CG285957 25-AUG-2003
CGMKG93TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0607P17,
genomic survey sequence.
CG285957.1 GI:34200171
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1 (bases 1 to 827)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Umpublished (2002)
Other_GSSS: OGWKG93TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 GCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGC 77
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 301-838-6208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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methylation filtered genomic DNA library"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TR
Class: sheared ends.
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Class: sheared ends.
Location/Qualifiers
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OGABBOITC ZM_0.7_1.5_KB Zea mays genomic clone ZMWBMa0020023, genomic survey sequence.
BZ410270
BZ410270.1 GI:26042544
GSS.
                                                                                                                                                                     BZ532489 654 bp DNA linear GSS 16-DEC-2002 OGAEY44TC ZM2_0.7_1.5 KB Zea mays genomic clone ZMMBMa0046G15, genomic survey sequence.
BZ532489 GI:27077191
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Zea mays
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Sherrycta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
     169 GTGAGCTTGGTGAGGCACTTGAGCCGGGCAACCTCCGCCAGTATGGAGCACGAGGATGGC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GCGCGCTCGCTCACTCAGCCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.7%; Score 34.6; DB 28; Length 654; Best Local Similarity 59.8%; Pred. No. 2.5e+02; Matches 58; Conservative 0; Mismatches 39; Indels 0;
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                                         78 CCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAG 114
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
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BZ532489
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/clone_lib="ZM_0.7_1.5_KB"
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9		
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ite_1: Hi omic_DNA		DB 29;
r: pBCSK-; S. filtered gen		27.7%; Score 34.6; DB 29; Length 827;
/note="Vecto methylation	•	27.78;
	ORIGIN	Query Match
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ö 18 GCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGC 77 0; Gaps Query Match
27.7%; Score 33.0, 72.02.,
Best Local Similarity 59.8%; Pred. No. 2.7e+02;
Matches 58; Conservative 0; Mismatches 39; Indels

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Search completed: April 1, 2004, 17:02:17 Job time : 1606.24 secs

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Perfect score:

Sequence:

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Run on:

Scoring table:

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Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS CDNA Library Preparation: Wei WU / Prof. Christof NIEHRS CDNA Library Preparation: Wei W. DKPZ CDNA Library Preparation: Wei W. A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT 15918074 XtSt10-30 Silurana tropicalis cDNA clone IMAGE:7027270 3', mRNA Sequence.
CF784470
CF784470.1 GI:37748315
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AL552621

BO048852

BO048852

BMS 0624

BMS 0624

BMS 0627

BY733594

AG060831

BX407619

CNS017V2

BM924606

AG080476

CC390088

CC390088

CC390088

CC390088
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CG365468
CG365468
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BM807831
BAC17628
BHC152072
BMC75072
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CF784470/c
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AUTHORS
TITLE
JOURNAL
COMMENT
  CF784470 AGENCOURT
BE495968 WHB1260 H
BZ569259 pacs2-164
AG185368 Pan trogl
                                                                                                                                               1, 2004, 14:50:59; Search time 1859.76 Seconds (without alignments) 2328.267 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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145
1 TIGGCCACTCCCTCTGCG......CTCCATCACTAGGGGTTCCT
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BE495968
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                                                                                                           nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_gss_fun:*
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Maximum DB seq length: 2000000000
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EST 20-OCT-2003

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/db_xref="taxon:4550"
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BZ569259.1 GI:27203589
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Pseudomonas aeruginosa
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l Similarity 57.9%;
66; Conservative
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56.7%;
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                                                                                                                                                                                                                                       /d_xel="taxonisor"/
/dlocate="taxonisor"/
/closue type="whole embryo, pool of stages 10, 20 and 30"
/tissue type="whole embryo, pool of stages 10, 20 and 30"
/tissue type="whole embryo, site_l: BamHI; Site_2: XhoI; 10 ug
/note="Vector: pxkw2; Site_l: BamHI; Site_2: XhoI; 10 ug
of poly4+ RNA was isolated from a mixture of embryos at
stage 10, 20 and 30 und primed by oligo-dr primer:
5-GAGAGAGAGAGACCTC(I)16VN-3' (where V=G,A,C).
5-methyl-dCTP was used instead of dCTP in the first strand
synthesis in order to get hemimethylated cDNA. After
full-length enrichment, oligo-dG tailing and normalization
sqainst itself, second-strand synthesis was carried out by
priming with 5'-GAGAGAGAGACTGAGATTAATTAATC(313-3' dSDNA
was digested with XhoI/SamHI and directionally cloned into
the pxkw2 vector. Average insert size is 1:5 kb. Library
constructed using the Carninci protocol (Genome Research
2000) by Drs. W. Wu and C. Niehrs (DKFZ, Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The structure and function of the expressed portion of the wheat genomes - Anther CDNA library from rye Unpublished (2000)
Unpublished (2000)
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 8800 Buchanan Street, Albany, CA 94710, USA
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Epermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Dooideae, Triticae, Secale.

1 (bases 1 to 304)
Anderson, O. D., Butler, E., Chao, S., Choi, D.W., Close, T.J.,
Anderson, N.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y.,
Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.6%; Score 38.6; DB 14; Length 974; 91.1%; Pred. No. 35; ive 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GAGCGCGCAGAGAGAGAGTGGCCAACTCCATCACTAGGGGTTCCT 145
  I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                            organism="Silurana tropicalis"
found through the I.M.A.G.E. Consorti
http://image.llnl.gov
Plate: LLAM14761 row: d column: 20
High quality sequence start: 36
High quality sequence stop: 157.
Location/Qualifiers
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/mol_type="mRNA"
                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:8364"
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/dev stage="Adult plant before anthesis"
/dev stage="Adult plant before anthesis"
/lab_host="E. coli SOLR"
/clone_lib="Secale cerale anther cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_l: EccRI; Site_2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late melosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) utiliversity of Missouri, columbia. A cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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pacs2-164_8319.x2r5p12 pacs2-164 Pseudomonas aeruginosa genomic
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1 (bases 1 to 1015)
Spencer, D. H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGGCCACTCCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCC
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/strain="2-164"
/bx.ref="taxon:287"
/clone="pocs2-164 8319"
/clone lpacs2-164 8319"
/clone lpacs2-164 8319"
/note="clinical isolate 2-164 Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37.8; DB 10; Length Pred. No. 38; 0; Mismatches 48; Indels
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 206687244
Email: craymond@u.washington.edu
Class: shotgun.
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Pred. No. 68;
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpessescrirken:go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-50-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                   noidosos
Pan troglodytes DNA, clone: RP43-059G23.TJ, genomic survey
sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                  4 GCCACTCCCTCTCTCTCCCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGA
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Toroki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
Unpublished
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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52; Indels
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
db_xref="taxon:9588"
/clone="RP43-059G23.TJ"
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68; Conservative
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ORN-GIORE F330012R6 5', mRNR sequence.

SIGN BY52719 KIRK full-length enriched, achit inner ear Wis musculus CORN-GIORE F330012R6 5', mRNR sequence.

MASSATS AND CICZISSISS CONTROLLS AND CORN-GIORE STATES AND CORN-GIORE F330012R6 5', mRNR sequence.

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EN (Dases 1 to 969)

In (Dases 1 to 969)

RS ii, W.B., Gruber.C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

AL Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12914687.

Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EDNA codex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2860.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODMO14DE06NP1&cluster=2860.r. Contact:

Feng Liang Email: fliang@lifetech.com URL:

Feng Liang Email: fliang@lifetech.com URL:

Location/Qualifiers

Location/Qualifiers
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                 prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital S55 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                             /dev_stāgē="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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Experimental Animal Research in Riken contributed
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/dev stage="fetal"
                                                                                                                                                1. .644
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1 Similarity 56.1%;
69; Conservative
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AL564360/c
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CNSOSGBJ 1121 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 003C03 of library B from Tetraodon nigroviridis, genomic survey
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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AL336088.1 GI:8229846
AL336088.1 GI:8229846

SS: genome survey sequence.

"
Tetraodon nigroviridis

Tetraodon nigroviridis

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii, Teleostei; Buteleostei; Neoteleostei;

Acauthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/mol_type="genomic DNA"
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14.0%; Pred. No. 1.2e+02;
ive 66; Mismatches 51;
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843 NSTSSASTSSTSSSS 828
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/moll_type="mrxn" orpton:
//moll_type="mrxn" orpton:
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/coll_line="RAWOS CELL LINE"
/clone="line="taxon orptions B CELLS (RAWOS CELL LINE)"
/note="line="taxon orptions B CELLS (RAWOS CELL LINE)"
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CG273564
CG273564.1 GI:34185705
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BX405071
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BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologias, a division of
Invitrogen. This sequence belongs to sequence cluster 10245.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAG006BD03NP1&cluster=10245.r. Contact :
Feng Liang Email : fliangalifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAG006BD03NP1.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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24.6%; Score 35.6; DB 13; Length 1201;
Best Local Similarity 43.8%; Pred. No. 1.9e+02;
Matches 56; Conservative 19; Mismatches 53; Indels 0;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BX405071
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1103)
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: sequefégenoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulliength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH12FP1.
/clone="003C03"
/clone lib="B"
/note="Genoscope sequence ID : COAB003AB02C1~end : T?"
                                                                                                                                                                                                                                                                                                       4 GCCACTCCCTCTCTGCGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGA
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                                                                                                                                                            Score 35.8; DB 29;
Pred. No. 1.7e+02;
0; Mismatches 72;
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l Similarity 47.1%;
64; Conservative
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(Dases 1 to 654)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Clessick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Cltek, R.W., Numberg, A., Robbins, D. and Lakey, N.
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                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
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Strain="873"

(b Strain="873"

/clone="EMMBMa0750D08"

/clone="WetCr: pBCSK-; Site 1: Hincl!; 0.7-1.5 kb

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                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Exx: 301-838-5208 Email: whitelaw@rigr.org Seq primer: TR
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Contact: Cathy Whitelaw
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BZ532489
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747 bp DNA linear GSS 04-DEC-2002
.XB Zea mays genomic clone ZMMBMa0020023,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Consortium for Maize Genomics
Unpublished (2002)
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methylation filtered genomic DNA library"
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Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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/ strain= B73"
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/ Clone="Lib="ZM" / 1.5 kB"
/ note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 hethylation filtered genomic DNA library"
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TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
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OGABBOITC ZM 0.7 1.5 KB Z
genomic survey sequence.
BZ410270
BZ410270.1 GI:26042544
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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CG441848 840 bp DNA linear GSS 17-SEP-2003 OG3DB09TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0779B18, genomic survey sequence.
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1 (bases 1 to 840)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OG3DB09TV
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/organism="zea mays"

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/organism="B7"

/strain="B7"

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methylation filtered genomic DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Sense Sens
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9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
      Consortium for Maize Genomics
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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CG441848.1 GI:34820478
                         Unpublished (2002)
Other GSSs: OG2BF05TV
Contact: Cathy Whitelaw
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Best Local Similarity 57.0.
Best Local Si Conservative
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CG2BF05TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0751B10,
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1 (Dases 1 to 827)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Numbers, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics and Lakey, N.

Consortium for Maize Genomics
Other GSS: OGWKG93TV
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Spermatophyta, Uiliopsida; Poales, Poaceae; PACCAD
Zelade; Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 839)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Zesnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
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methylation filtered genomic DNA library"
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      533 CTGGGCGCCACCATTGAGAGCTCGAGCTCCTTGAGAGCCTGCATCCGAC 485
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1 Similarity 57.8%; Pred. No. 1.98+02;
63; Conservative 0; Mismatches 46; Indels 0;
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9712 Medical Center Drive, Rockville, MD 20850, USA
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/organism="Zea mays"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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CG365468
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methylation filtered genomic DNA library"
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Search completed: April 1, 2004, 17:02:14 Job time : 1875.76 secs

us-10-620-039-1.rnpb

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APPLICANT: Bahou, Wadie
APPLICANT: Bandalon, Daiv
APPLICANT: Gandalon, Daiv
TILE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SENGTH: 145
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Matches 145; Conservative
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Sequence 8, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 58, Appl
Sequence 26, Appl
Sequence 36, Appl
Sequence 33, Appl
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                                                                                                                                                                                                                                     April 1, 2004, 16:04:14; Search time 218.574 Seconds (without alignments) 2480.895 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 31,
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1 TTGGCCACTCCCTCTGCG......CTCCATCACTAGGGGTTCCT 145
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2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-792-378A-8
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Listing first 45 summaries
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                                                                                                                                                               OM nucleic - nucleic search, using sw model
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-845	US-09-845-416-30		-782-	3 - 240 - 198	58	9-804-898	ĭ	US-10-038-97	US-10-136-819-	US-10-077-294	US-10-163-886-	US-10-263-12	US-10-375-777-	US-10-696-261-1	US-10-696-282-1	US-10-696-900-1	US-10-696-		US-10-696-900-1	US-09-845-416-2		US-09-845-416-3	US-09-845-416-	US-09-845-416-2	US-09-845-416-3	US-09-845-416-3	US-09-845-416-3	US-09-845-416-3	US-09-845-416-27	
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ALIGNMENTS

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Gaps

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Length 145; Indels

100.0%; Score 145; DB 9; 100.0%; Pred. No. 1.6e-32; tive 0; Mismatches 0;

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121 GCCAACTCCATCACTAGGGGTTCCT 145
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; ORGANISM: Adeno-associated virus
US-10-159-968-13
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Matches 145; Conservative
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ORGANISM: Unknown
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APPLICANT: Anton J. Cathomen
TITLE OF INVENTION: METHOD OF IDENTIFYING CELLULAR
TITLE OF INVENTION: METHOD OF DENTIFYING CELLULAR
TITLE OF INVENTION: MECHOD OF ADENO-ASSOCIATED VIRUS (AAV)
FILE REFERENCE: SALKINS: 041A
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: 60/286951
PRIOR APPLICATION NUMBER: 60/286951
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 146
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Best Local Similarity 100.0%; Score 145; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.66-32;
Matches 145; Conservative 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 27; SOFTWARE: Patentin Version 3.0

SEQ ID NO 8: SEQ ID NOS: 27
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                                                                                                                                                                  S-10-135-984-8 .
Sequence 8, Application US/10135984 Publication No. US20020182595A1 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-782-378A-8
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US-09-782-378A-8
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; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 of U.S. Patent No. US20020197237A1 5,478,745
US-10-054-665-7
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iSequence 13, Application US/10159968

iSequence 13, Application US/10159968

iPublication No. US20030152914A1

iGENERAL INFORMATION:

APPLICANT: Musacov, Serge

iTILE OF INVENTION: Method for Generating Replication

iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

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iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

iTILE OF INVENTION: Defective Viral Vectors That are Helper Free

iTILE OF INVENTION VIMBER: US 60/294,797

iPRIOR APPLICATION NUMBER: US 60/294,797

iPRIOR FILING DATE: 2001-08-07

iPRIOR 
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Sequence 7, Application US/10054665

Publication No. US20020197237A1

GENERAL INFORMATION:

APPLICANT: Engelhardt, John F.

APPLICANT: Duan, Dongsheng

TITLE OF INVENTION: Adeno-associated virus vectors

FILE REPERENCE: 875.007US2

CURRENT APPLICATION NUMBER: US/10/054,665

CURRENT FILING DATE: 2002-06-13

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSRQ for Windows Version 4.0

SEQ ID NO 7.
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TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DE142
CURRENT FILING DATE: 2001-04-30
PRIOR PILING DATE: 2001-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 955
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Publication No. US2033171312A1

GENERAL INFORMATION:
APPLICANT: XIAO, XIAO

TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DE1142
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                                                                                                                                                                                                                                                                                   Length 207;
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 58
; LENGTH: 207
; TYPE: DNA
; PRATURE: DNA
; FRATURE:
; CTHER INFORMATION: Synthetic enzyme attachment site sequence
US-10-023-208-58
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ilarity 100.0%; Pred. No. 1.2e-32;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                100.0%; Score 145; DB 14;
100.0%; Pred. No. 1.5e-32;
ive 0; Mismatches 0;
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Publication No. US20030171312A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 145; Conservative
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; ORGANISM: Homo sapiens
US-09-845-416-26
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Matches 145; Conserv
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-09-845-416-26
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US-10-276-356-1/C
US-10-276-356-1/C
Sequence 1, Application US/10276356
Publication No. US20040029106A1
GENERAL INFORMATION:
APPLICANT: Damalstiv of No. US20040029106A1th Carolina at Chapel Hill
APPLICANT: Samulstiv R. Jude
APPLICANT: McCarty, Douglas M.
TITLE OF INVENTION: DUPLEXED PARVOVIRUS VECTORS
FILE REPRENCE: 5470-282
CURRENT APPLICATION NUMBER: US/10/276,356
CURRENT FILING DATE: 2001-05-31
PRIOR PILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
LENGTH: 175
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Publication No. US20030124537A1
GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Wan-Ching
TITLE OF INVENTION: PROCARYOUT LIBRARIES AND USES
FILE REPERENCE: A-70174-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/023,208
CURRENT FILING DATE: 2001-12-17
PRIOR PILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 63
                                          100.0%; Score 145; DB 14;
100.0%; Pred. No. 1.6e-32;
ive 0; Mismatches 0;
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                                                                    al Similarity 100.
145; Conservative
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US-10-023-208-58
                                          Query Match
Best Local S
Matches 145
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US-09-845-416-33
; Sequence 33, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DAN SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFRENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR PILLING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOOFWARE: Patentin Ver. 2.1
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100.0%; Score 145; DB 10; Length 987;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 145; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                         Length 955;
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                                                                                                                                                                                                                     Query Match
100.0%; Score 145; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 145; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT FILING DATE: 2001-04-30
PRIOR PLILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 955
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US-09-845-416-26
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LENGTH: 987
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RESULT 11
US-09-845-416-33/c
; Sequence 33, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
APPLICANT: XIAO, XIAO

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| Sequence 3.2 Application US/09845416|
| Publication No. US20030171312A1|
| Publication No. US20030171312A1|
| GENERAL INFORMATION:
| APPLICANT XIAO, XIAO
| TITLE OF INVENTION: THEREOF|
| TITLE OF INVENTION: THEREOF|
| FILE REPRENCE: DB1142|
| CURRENT APPLICATION NUMBER: US/09/845,416|
| FILE REPRENCE: DB1142|
| PRICR FILING DATE: 2001-04-30|
| PRICR FILING DATE: 2000-04-28|
| NUMBER OF SEQ ID NOS: 36|
| SOFTWARE: PatentIn Ver. 2.1|
| SEQ ID NO 32|
| LINGTH: XIA414|
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TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE TITLE OF INVENTION: THEREOF ENCODING A DYSTROPHY MINIGENE AND USE FILE REFERENCE: DELIA.

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT FILING DATE: 2001-04-30

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.1

LENGTH: 987
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100.0%; Score 145;
Best Local Similarity 100.0%; Pred. No. 9
Matches 145; Conservative 0; Mismatche
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US-09-845-416-32/c
; Sequence 32, Application US/09845416
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CORGANISM: Homo sapiens
US-09-845-416-33
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ORGANISM: Homo sapiens
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US-09-845-416-31
Sequence 31. Application US/09845416
Publication No. US20030171312A1
SEQUENCE INPORMATION:
APPLICANT XIAO, XIAO
TITLE OF INVENTION: THRREOF
TITLE OF INVENTION: THRREOF
TITLE OF INVENTION: THRREOF
TITLE OF INVENTION: US/09/845,416
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT FILING DATE: 2001-04-30
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 31
LENGTH: 4476
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Publication No. US20030171312A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIAO, XIAO,
TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF
FILE REPERENCE: DEILAL
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT FILING DATE: 2001-04-30
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PARENCE TOWN OF 2.1
SEQ ID NO 3.2
LENGTH: 4414
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CORGANISM: Homo sapiens
US-09-845-416-32
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Fublication No. US20030171312A1
GENERAL INFORMATION:
APPLICANT: XIAO,
ITILE OF INVENTION: THEREOF
FILE REPERBUCE: DB1142
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT PILING DATE: 2001-04-30
FRIOR PILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 4476
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Job time : 229.574 secs
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US-09-845-416-31
RESULT 15
JS-09-845-416-31/c
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April 1, 2004, 12:58:58; Search time 210.185 Seconds (without alignments) 2526.461 Million cell updates/sec
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125
1 TIGGCCACICCTCTCTGCG.......CGCAGAGGGAGGGAGTGGCCAA 125
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Result	به	Query				
No	Score	- 1	Length	8	QI	Description
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-	4 12	_		w	ABS69886	Abs69886 Human ade
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	υυ		RESI ID XX	Z X	E X	님 :	{₹}	8 \$	8 E S	(요)	4 H S	\$ E \$	4 E S	4 II X	省	4222	283	\$888888888888

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inverted terminal repeats. The vector is safe for use in gene therapy, partite, in treatment of haemoglobinopathies and a variety of diseases, e.g. thalassemia, diabetes, sickle cell anaemia, and cancer. See also AAQ41449. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                       139
                                                                                                                                                                                                                             Adeno-associated virus-2 basal vectors - for gene therapy and treatment of haemoglobinopathies and cancer etc. - has cassette contg. a promoter capable of cell-specific expression, between 2 inverted terminal repeats of the adeno-associated virus 2.
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                                                                                                                                                CTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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note= "inverted terminal repeat forming palindromic
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                                                                  Length 144;
                                                                                                        Indels
                      A; 49 C; 52 G; 20 T; 0 U; 0 Other;
                                                           .Match 100.0%; Score 125; DB 8; Local Similarity 100.0%; Pred. No. 1.2e-23; es 125; Conservative 0; Mismatches 0;
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/*tag= b
/note= "Flip orientation"
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(first entry)
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                          Sequence 144 BP; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inverted terminal repeat, ITR; adenovirus; adeno-associated virus; AAV-2; replication defective; integration; gene therapy; ds.
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                                                                                                                                                                                                                                                                                Recombinant defective adenovirus contg. integratable expression casset - for use in gene therapy to express protein, antigen or antisense nucleic acid, also for prodn. of recombinant adeno-associated viruses.
                                                                                                                                                                  TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGAACGTCGCC
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                                                       145;
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                                                                                                           Indels
                                                    Length
Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
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                                                 Query Match

100.0%; Score 125; DB 2;

Best Local Similarity 100.0%; Pred. No. 1.2e-23;

Matches 125; Conservative 0; Mismatches 0;
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18-APR-1996
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WPI; 1997-192917/17
(AVIG-) AVIGEN INC.
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                                  Gaps
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 Length 145;
                                0; Indels
 Score 125; DB 2;
Pred. No. 1.2e-23;
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1. label= Rep_binding_site
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53. 61
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'note= "region D"
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AAT63408 standard; DNA; 145 BP.
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               Best Local Similarity 100.
Matches 125, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adeno associated virus.
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Best Local
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The present sequence is the inverted terminal repeat (ITR) from the wild type adeno associated virus (AAV) serotype 2 genome. A novel nucleic acid construct, comprises a targetting sequence capable of binding AAV Rep, e.g. the present sequence, and at least 1 heterologous nucleotide sequence arranged relative to the targetting sequence, so that it is integrated into a target site in a recipient genome. The integration system can be used to integrate a selected nucleotide sequence into a recipient cell genome, useful in the treatment of an acquired or inherited disease, e.g. long term gene therapy. The integration system in regard to the size of the nucleotide sequence to be delivered and does not result in the integration of viral gene sequences into the recipient cell genome. Specifically it can be used to safely and efficiently deliver, and integrate large nucleotide sequences into a disciplant erighent cell genome without the risk of causing insertional mutagenesis due to random integration events
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                                                                                                                                           Nucleic acid construct for integration into target site in recipient genome - comprises target sequence to bind AAV Rep and heterologous nucleotide sequence, for treatment of acquired or inherited disease.
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100.0%; Score 125; D
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 125; Conservative 0; Mismatches
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Natsoulis G, Surosky RT;
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20-APR-2000; 2000GB-00009887.
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                                                                                                                      Beard PM;
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                                                                                                                                                                                                                                                                                                                                  associated virus (AAV) vectors comprising a promoter e.g. an AAV promoter (AAX34296) and a selected DNA sequence, especially an AAV rep gene and a parvovirus B19 cap gene, located between 2 AAV inverted terminal repeats (ITR) such as the ITR sequence shown here. The system can specifically target primitive progenitor and differentiated cells of the erythroid lineage, and can achieve stable integration and expression of transduced genes. The vectors can be used for the in vitro or in vivo delivery of genes to cells such as bone marzow cells, peripheral blood cells, endothellal cells and myocardial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 125; DB 2; Length 145; 100.0%; Pred. No. 1.2e-23; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                           The invention relates to new recombinant chimeric
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                                                                                                                                                                                     New recombinant adeno-associated vectors
(ADRE-) ADVANCED RES & TECHNOLOGY INST.
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/note= "unpaired base"
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/note= "unpaired base"
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1. .145
                                                                                                                                                                                                                                             Claim 2; Page 69; 76pp; English.
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                                                        Srivastava A, Ponnazhagan S;
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(first entry)
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Best Local Similarity 100.
Matches 125; Conservative
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The invention relates to single stranded and/or looped DNA having a portion with at least one base, internally located with respect to any 3' and 5' ends of the DNA, that is unbasepaired with another base in a form that is capable of being internalised within a target cell, for use in therapy, with cytostatic and virucide activity. The DNA acts as an application in cells that lack p53 functionality, useful for application preferably a dividing cell where the cell is other than a seaso-tent that selectively kills the cell. The DNA is preferably in the protein that selectively kills the cell. The DNA is preferably in the form of an AAV or associated with AAV protein which has been treated such that the DNA is no longer capable of replication or expression in cells and is associated with or contained within a vehicle which is associated with one or more viral fibers which facilitate internalisation of the DNA into a target cell. The DNA is also useful for manufacturing a medicament for treating an individual suffering from a mutant p53 associated cancer can infection that inhibits cellular by a mutant p53 associated cancer can infection that inhibits cellular by such as full or handled and no damage to cells infected with p53 inhibiting viruses, such as HPV16 or HPV18 and only cells that lack p53 activity are killed and no damage to cellular DNA is involved. The present sequence is that of the adenosassociated virus (AAV) 2 ITR, the double loop structure found at each end of the AAV DNA. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                      Single stranded and/or looped DNA for treating mutant p53 associated cancer or infection that inhibit cellular p53, having portion with an base, internally located with respect to any 3' and 5' ends of the DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Page 38; 51pp; English.
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(BTGI-) BTG INT LTD
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The present sequence is that of an adeno associated virus (AAV) palindromic inverted terminal repeat (ITR) region. An AAV ITR is used in novel insect cell-compatible vectors of the invention that are designed for the production of AAV in insect cells. The vectors comprise an AAV ITR and coding sequences for AAV VP1, VP2 and VP3 capsid proteins, for AAV non-structural replication (Rep) proteins Rep52 or Rep40, and for AAV Rep78 or Rep68. The method of producing AAV in insect cells provides an efficient, safe and economical means of producing a large amount of recombinant AAV particles which may be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing an adeno-associated virus (AAV) in an insect cell, e.g. for gene therapy, comprises introducing an insect cell-compatible vector into an insect cell and maintaining the insect cell under conditions that
                                                                                                                                  AAV; inverted terminal repeat; insect; gene therapy; vector; ss.
                                                                              Adeno associated virus inverted terminal repeat region.
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                                                                                                                                                                                                                                           Location/Qualifiers
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13-AUG-2002; 2002US-00216870.
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/*tag= a
                                                                                                                                                                                       Adeno associated virus.
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                          26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (NS) having 5' and 3' end, left and right inverted terminal repeats of adenovirus flanking NS, adenovirus packaging sequence linked to inverted terminal repeat, and adeno-associated virus terminal repeat linked to 3' end of NS, into cell expressing adenovirus early gene lacking from vector and culturing cell to produce another vector. The method is useful for generating vectors, especially mAd vectors. The method is useful in transferring nucleotide sequences of interest into a cell, for gene transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo. The nucleotide sequences are useful for treating diseases associated with it, i.e. adenosine deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deficiency with severe combined immune deficiency, beca-chain of haemoglobin gene associated with beta-thalassaemia and sickle cell disease, receptor for low density lipoprotein gene associated with familial hypercholesterolaemia, hypoxanthine-guanine phosphoribosyltransferase associated with Lesch-Nyhan syndrome, phenylalanine hydroxylase (PAH) gene associated with phenylketonuria, dystrophin gene associated with muscular dystrophy, and human cystic fibrosis transmembrane conductance regulator gene associated with cystic fibrosis. The present nucleic acid sequence represents a human adenoassociated virus 2 (AAV2) terminal repeat sequence that was used in the
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antianaemic; antilipaemic; nootropic; cytostatic; dermatological;
human adeno-associated virus 2; AAV2; terminal repeat; ds:
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100.0%; Score 125; DB 6; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                  US2002102731-A1.
                                                                                 Homo sapiens.
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                                                          1 TTGGCCACTCCCTCTCTGCGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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 Length 145;
                              0; Indels
Query Match
100.0%; Score 125; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                      ACF35876 standard; DNA; 145
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                                                                                                                                                                                                                                                         ACF35876
ID ACF3
XX
AC ACF3
XX
DT 06-N
XX
                                                                                                                                                                                                                                             RESULT 9
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GCCAA 125 GCCAA 125

61

셤 ઠે 셤 ò ద 8491/c ACC58491 standard; DNA; 145 BP.

RESULT 8 ACC58491/c ID ACC5: XX

ACC58491;

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misc_binding
 The invention relates to a recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed. A complete virus-mediated system for recombinant AAV production is provided which comprises: (a) a first recombinant adenovirus encoding one or more AAV REP78/68 polypeptides and one or more agene of interest and AAV inverted terminal repeats that flank the of interest; (c) viral helper functions; and (d) a host cell comprising the first recombinant adenovirus, the second recombinant adenovirus, and the viral helper functions; the second recombinant adenovirus, and the viral helper functions. The recombinant AAV is useful as a vector for gene therapy. The present sequence represents an AAV-2 left inverted terminal repeat (ITR) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                              wew recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed, useful as a vector for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGGGGACCAAAGGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ceaceccedecririoccedecercreacidadeceaecedeaecedaaaaaaaaagaagre
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inverted terminal repeat, Rep recognition sequence, AAV-2, ss, RRS, viral regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                   Length 145;
           ds.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
           Adenovirus; Rep78; Rep68; CAP; gene therapy; AAV-2; ITR;
                                                                                                                                                                                                                                                                                                                                                                               Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adeno-associated virus-2 inverted terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 125; DB 8;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adeno-associated virus serotype 2.
                                                                                                                                                                                                                              Example; Page 120; 122pp; English.
                                                                                       17-JAN-2003; 2003WO-US001624.
                                                                                                           18-JAN-2002; 2002US-0349532P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX93568 standard; DNA; 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                             Adeno associated virus
                                                                                                                                                                     WPI; 2003-627412/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GCCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GCCAA 125
                                                                                                                             (UYDU-) UNIV DUKE
                                                WO2003061582-A2
                                                                                                                                                Zhang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2003
                                                                    31-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX93568;
                                                                                                                                                 Li C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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The invention relates to identifying molecules that interact with an aden-associated viral regulatory element (e.g.a Rep recognition sequence, RSD comprising contacting at least one molecule with a nucleic sequence, RSD comprising contacting at least one molecule is bound to the viral regulatory elements. Also included is a kit for analysing the interaction between molecules and an adeno-associated viral regulatory element. The method is useful for identifying molecules e.g. at least one cellular protein, recombinant proteins, synthetic protein or exogenous protein (preferably human proteins that are derived from a cDNA library or cellular lysate), or peptide, antibody, nucleic acid, lipid, carbohydrate and/or organic or inorganic compound that interacts with an adeno-associated virus (AAV) and facilitates the application of adeno-associated virus-based vector system, therefore ITR-binding of adeno-associated virus-based vector system, therefore ITR-binding proteins and other molecules provide new insights into the AAV life cycle, including the regulation of gene expression and integration, and suggests improvements for its application in thereapy. The present is an AAV-2 ITR containing an RRS used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of cellular regulations of adeno-associated virus involves contacting an adeno-associated viral regulatory interacting molecule with a nucleic acid comprising a adeno-associated viral regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= f bound moiety= "Nucleotides 41-1 of the present sequence" 3. \cdot .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= g
/label= Rep_recognition_sequence
/note= "This RRS is specifically claim in claim 13"
122. .127
1. .41
/*tag= a
/bound_moiety= "Nucleotides 125-85 of the present
                                                                                                                                                                                                                                            4. .62
*tag= c
bound_moiety= "Nucleotides 50-42 of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= e
'bound moiety= "Nucleotides 72-64 of the present
                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
/bound_moiety= "Nucleotides 84-76 of the present
                                                                                                                                                                              "Nucleotides 62-54 of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= h
/label= Terminal_resolution_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 16pp; English
                                                                                                                                            /*tag= b
/bound_moiety= "
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-APR-2002; 2002US-00135984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-2001; 2001US-0286951P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weitzman MD, Cathomen AJ;
                                                                                                                                                                                                                                                                                                                                               sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence"
                                                                                  sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WEIT/) WEITZMAN M (CATH/) CATHOMEN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002182595-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                 misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_signal
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셤 ઠે 셤 δ 셤

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/*tag= m
//abel= Double-D
//abel= Double-D
//abel= This 165 bp sequence, resulting from addition of
a second D reset to the AAV ITR, has not been identified
in any naturally occurring virus!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type= INVERTED
/label= D_repeat
/label= D_repeat
/label= T-shaped
/label= T-shaped structure for DNA replication when single
-stranded"
                    /*tag= .c
/rpt_type= INVERTED
/label= A/_repeat
/note= "Forms the stem of a T-shaped structure when base
paired with repeat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adeno associated virus inverted terminal repeat with double D region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= j
/note= "Part of T-shaped structure, formed by base
paring between the C' and C repeats"
63. .70
/*tag= d
/rpt type= INVERTED
//rpt - repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= k
/note= "Part of T-shaped structure, formed by base
paring between the B' and B repeats"
85. .92
                                                                                                                                                                                                                                                                          Viral replication, REP protein, inverted terminal repeat; ITR, adeno-associated virus; AAV, vector; double-D; cis-acting; lytic life cycle; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .dg= e /rpt_type= INVERTED /label= C_repeat +tp.
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                          AAT49462 standard; DNA; 165 BP.
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                   Adeno associated virus.
                                                         121 GCCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_structure
                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                  10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_unit
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                                                                                                                                                                                                                                                                                                                                                   Synthetic.
   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stem_loop
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                                                                                                                                                                                      AAT49462;
                                                                                                                                RESULT 12
                                                                                                                                              AAT49462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The 20-bp D-sequence given in AAQ66773 is present in the inverted terminal repeat (ITR) sequence of AAV and is required for viral replication. A novel, modified terminal repeat structure, double-D ITR, was constructed (AAQ66769) that contained a single 145 bp ITR sequence with an additional D' sequence. The double-D ITR fragment allows proteins an encapsial action of encapsial accombinant DNA into AAV capsid proteins. Vectors including double-D ITR can be used for gene replacement therapies. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                              ceacecceegerrrececeegecercreagreagecaageceegegagag 120
                                                                                                                                                               TIGGCCACTCCCTCTCTGCGCGCGCTCGCTCGCTCAGGCCGGGGGCCGAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGAACGACGAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-D ITR; inverted terminal repeat; D-sequence; AAV; adeno-associated virus; capsid; encapsidation; gene therapy; vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenovirus associated viral inverted terminal repeat - for use in recombinant viral vector system for treatment of genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
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                          100.0%; Score 125; DB 7; Length 146; llarity 100.0%; Pred. No. 1.2e-23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 125; DB 2; Length 1 Best Local Similarity 100.0%; Pred. No. 1.2e-23; Matches 125; Conservative 0; Mismatches 0; Indels
Seguence 146 BP; 21 A; 53 C; 49 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 25; 44pp; English.
                                                                                                                                                                                                                                                                                                      AAQ66769 standard; DNA; 165 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-00989841.
                                                                                                                                                                                                                                                                                                                                                                                                           Double-D ITR terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-US011728.
                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPI-) UNIV PITTSBURGH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Samulski RJ, Xiao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-217868/26.
                                        Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                      GCCAA 125
                                                                                                                                                                                                                                121 GCCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9413788-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
20-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                   AAQ66769;
                                                                                                                                            19
                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                           Query Match
                                                                                                                                                                                                                                                                                        AAQ66769
ID AAQ6
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à g RESULT 13

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The adeno associated virus (AAV) has a 145 bp inverted terminal repeat (ITR) located at each end of its genome. In addition to being able to base pair with each other, the ITRs can also individually fold back on the selves through the base pairing of A, A', B, B' and C, C' sequences to form a T-shaped structure for DNA replication (see features table). It has been found that viral mutants with deleted D sequences are unable to replicate their DNA. Addition of a second D repeat (D') to the naturally occurring ITR resulted in a sequence, designated double-D, which was sufficient to carry out the functions normally required of two wild-type in sufficient to carry out the functions normally required of directing replication and assembly into AAV, and/or the integration into the host genome, of recombinant DNA containing the mucleic acid molecule. Vectors and viral particles containing the double-D sequence are useful in gene therapy. Replication and integration into the host genome is completely effected through the double-D sequences, ensuring that the heterologous
                                                                                                                          /_v== ...
/rpt_type= INVERTED
/label= A repeat
/note= "Forms the stem of a T-shaped structure when base
paired with A' repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Double-D sequence directs adeno-associated virus integration into host genome - used in gene therapy, maintains full length coding sequence of therapeutic gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     /note= "Additional D' sequence"
                                                  /*tag= g
/rpt_type= INVERTED
/label= B'_repeat
104..145
/rpt_type= INVERTED
/label= B_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 9; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                     96WO-US006786
                                                                                                                                                                                                                                                                                                                                                                                       95US-00440738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene sequences remain intact
                                                                                                                                                                                                                    /*tag= i
/label= D'
                                                                                                                                                                                                      .165
                                .103
                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                       (SAMU/) SAMULSKI R J. (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Samulski RJ, Xiao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-042643/04.
                                                                                                                                                                                                                                                                                       WO9636364-A1
                                                                                                                                                                                                                                                                                                                                                        14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1995;
                                                                                                                                                                                                                                                                                                                      21-NOV-1996.
                                    repeat_unit
                                                                                                   repeat_unit
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9
                                                                                                21 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACGGCCGGGCGACCAAAGGTCGCC 80
                                                                            TTGGCCACTCCCTCTGCGCGCCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                        0; Gaps
  Length 165;
                                        0; Indels
100.0%; Score 125; DB 2;
100.0%; Pred. No., 1.2e-23;
iive 0; Mismatches 0;
Query Match
Best Local Similarity 100.0%;
Matches 125; Conservative C
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GCCAA 125 ||||| GCCAA 145

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The patent discloses a composition comprising at least two recombinant adeno-associated viruses (rAAVs). Each rAAV contains a recombinant DNA molecule comprising three DNA segments linked together. The first and the third DNA segments comprises 5' and 3' inverted terminal repeats (ITRs) respectively from the circular intermediate of AAV. The second DNA segment in each virus is different and does not comprise AAV sequence. It preferably comprises sequences encoding a therapeutically effective polypeptide such as the cystic fibrosis transmembrane conductance receptor gene (CTRR), the erythropoietin (epo) gene, the tyrosine hydroxylase gene (Parkinson's syndrome) or the glucocere-brosidase gene (Gaucher's disease). The circular intermediate of AAV imparts increased episomal stability and persistence of the vector in the host cell. Compositions comprising rAAV sequences are useful for transferring recombinant vector is useful in medical therapy, which includes the recombinant vector is useful in medical therapy, which includes treatment or prophylaxis of blood disorders such as Alzheimer's disease, parkinson's disease, muscle disorders involving skeletal, cardiac or smooth muscle ABV vector is used as a delivery vehicle for gene therapy. The present sequence is the ITR DD DNA sequence referred to as "doubbe sequence". This sequence is the ITR DD DNA sequence referred to 5',478,745. This sequence is not used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                             Recombinant adeno-associated virus; rAAV; circular intermediate; ITR; inverted terminal repeat; haemostatic; antisickling; neuroprotective; antianaemic; noctropic; blood disorder; sickle cell anaemia; thalassaemia; neurological disorder; haemophilia; Alzheimer's disease; muscle disorder; Parkinson's disease; gene delivery; erythropoietin; epo; CFTR; cystic fibrosis transmembrane conductance receptor; tyrosine hydroxylase; glucocerebrosidase gene; Gaucher's disease; gene therapy; Double DD; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition for transferring recombinant DNAs and to express a
polypeptide in a host cell, comprises two recombinant adeno-associated
virtuses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                           inverted terminal repeat double DD DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engelhardt JF, Dongsheng D, Ziying Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 139; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1999; 99US-0158209P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-2000; 2000WO-US027863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
(ENGE/) ENGELHARDT J F.
(DONG/) DONGSHENG D.
(ZIYI/) ZIYING Y.
               AAD03535 standard; DNA; 165
                                                                                                  19-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-266321/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           WO200125465-A1.
                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2001.
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Matches 125;
                                                           AAD03535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
AAD0353
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The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (NS) having 5, and 3 end, left and right inverted terminal repeats of adenovirus flanking NS, adenovirus packaging sequence linked to inverted terminal repeat of adenovirus packaging sequence linked to inverted terminal repeat linked to 3. and culturing cell to produce another vector. The method is useful for generating vectors, especially mad vectors. The method is useful in transferring nucleotide sequences of interest into a cell, for gene transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo. The nucleotide sequences are useful for treating diseases associated with it, i.e. adenosine deaminase gene associated with adenosine deaminase deficiency with severe combined immune deficiency, beta-chain of the amenglobin gene associated with beta-thalassaemia and sickle cell disease, receptor for low density lipoprotein gene associated with the familial hypercholesterolaemia, hypoxanthine-guanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenosine deaminase deficiency; severe combined immune deficiency; PAH; beta-chain, haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; phenylalamine hydroxylase gene; gene therapy; phenylkenouvia; phenylalamine hydroxylase gene; gene therapy; phenylkenouvia; dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antianaemic; antilipaemic; nootropic; cytostatic; dermatological; human adeno-associated virus 2; AAV2; terminal repeat; ds.
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                              21 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
  Tradeceactecereracedecreerregereacteaerregecegaceaaceaacece
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adeno-associated virus 2 terminal repeat DD sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 191pp; English.
                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000; 2000US-0237747P.
                                                                                                                                                                                                                                                                                                               ABS69886 standard; DNA; 165
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-690619/74.
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                                                                                                                                                                                                                                                                                                 140
phosphoribosyltransferase associated with Lesch-Nyhan syndrome, hencylalanine hydroxylase (PAH) gene associated with phenylketonuria, dystrophin gene associated with muscular dystrophi, and human cystic fibrosis transmembrane conductance regulator gene associated with cystic fibrosis. The present nucleic acid sequence represents a human adeno-associated virus 2 (AAV2) terminal repeat sequence that was used in the methods of the invention
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                                                                                                                                                                                                                                                     21 TIGGCCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCCAAAGGTCGCC
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                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of pTRT, a circular adeno-associated virus.
                                                                                                                                                               Query Match
100.0%; Score 125; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Circular adeno-associated virus; cAAV; replication; hairpin;
                                                                                                                                   T; 0 U; 0 Other;
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                                                                                                                                     Sequence 165 BP; 24 A; 59 C; 53 G; 29
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Sequence 31,

Sequence 31, Appl Sequence 30, Appl Sequence 1, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 28, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 36, Appli Sequence

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US-09-845-416-31

US-09-845-416-30

US-09-845-416-30

US-09-845-416-30

US-09-782-378A-1

US-10-240-198-1

US-10-240-198-1

US-10-240-198-1

US-10-240-198-1

US-10-240-198-1

US-10-240-198-1

US-10-240-198-1

US-10-240-198-1

US-10-136-818-1

US-10-136-818-1

US-10-136-818-1

US-10-136-818-1

US-10-66-282-18

US-10-696-282-18

US-10-696-282-18
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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   US-09-928-158B-1
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Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 17, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 26, Appli
                                                                         April 1, 2004, 16:04:14; Search time 188.426 Seconds (without alignments) 2480.895 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                     US-10-620-039-1_COPY_1_125
125
1 TTGGCCACTCCCTCTGCG......CGCAGAGAGGAGGGCCAA 125
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12 (GGDZ 6 ptodata/1/pubpna/US07 NEW PUB. seq:*

13 (GGDZ 6 ptodata/1/pubpna/US06 NEW PUB. seq:*

14 (GGDZ 6 ptodata/1/pubpna/US06 PUBCOMB. seq:*

15 (GGDZ 6 ptodata/1/pubpna/DS06 PUBCOMB. seq:*

16 (GGDZ 6 ptodata/1/pubpna/US08 NEW PUB. seq:*

17 (GGDZ 6 ptodata/1/pubpna/US08 NEW PUB. seq:*

18 (GGDZ 6 ptodata/1/pubpna/US08 PUBCOMB. seq:*

19 (GGDZ 6 ptodata/1/pubpna/US08 PUBCOMB. seq:*

10 (GGDZ 6 ptodata/1/pubpna/US09 PUBCOMB. seq:*

11 (GGDZ 6 ptodata/1/pubpna/US09 NEW PUB. seq:*

12 (GGDZ 6 ptodata/1/pubpna/US09 NEW PUB. seq:*

13 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

14 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

15 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

16 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

17 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

18 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

19 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

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11 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

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13 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

14 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

17 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*

18 (GGDZ 6 ptodata/1/pubpna/US108 PUBCOMB. seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-732-378A-6

US-10-120-198-2

US-10-135-984-8

US-10-135-984-8

US-09-782-378A-8

US-10-159-685-7

US-10-276-356-1

US-10-276-356-1

US-10-23-208-58

US-09-845-416-26

US-09-845-416-26

US-09-845-416-33

US-09-845-416-33

US-09-845-416-33

US-09-845-416-32

US-09-845-416-32
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                                                                                                                                                                                                    2465228 segs, 1869859620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match
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Sequence 1, Application US/09928158B
Patent No. US20202017222A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 102182-18
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/09/928,158B
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/224,132
PRIOR PLING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE Patentin version 3.0
SEQ ID NO 1
LENGTH: 130
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Sequence 33, Sequence 32, Sequence 32,

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Matchew D. Weitzman
APPLICANT: Matchew D. Weitzman
APPLICANT: Anton J. Cathomen
TITLE OF INVENTION: METHOD OF IDENTIFYING CELLULAR
TITLE OF INVENTION: REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
PILE REFERENCE: SALKINS.041A
CURRENT APPLICATION NUMBER: US/10/135,984
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/286951
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 125; DB 13; Length 146; Best Local Similarity 100.0%; Pred. No. 1.3e-25; Matches 125; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Bandalon, Ziv
APPLICANT: Gardalon, Ziv
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYES-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2000-102-12
PRIOR APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEO ID NOS: 27
SOFTWARE: Patentin version 3.0
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Publication No. US20020182595A1
GENERAL INFORMATION:
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; ORGANISM: adeno-associated virus
US-10-135-984-8
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100.0%; Pred. No. 1.3e-25;
cive 0; Mismatches 0;
Sequence 6, Application US/09782378A; Sequence 6, Application US/09782378A; Patent No. US20020102731A1
GENERAL INFORMATION:
APPLICANT: Hearing, Farrick
APPLICANT: Bandou Wadie
APPLICANT: Bandoun, Ziv
APPLICANT: Bandoun, Ziv
APPLICANT: Gandenko, Dmitzi
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYS-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2000-10-02.12
FRIOR APPLICATION NUMBER: 60/237,747
FRIOR APPLICATION NUMBER: 60/237,747
SPRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH 1.6
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Publication No. US20030100115A1
GENERAL INFORMATION:
APPLICANT: BTG INTERNATION:
APPLICANT: BTG INTERNATION:
APPLICANT: BTGAND R, PETER
APPLICANT: BTGAND R, RENNETH
ITLE OF INVENTION: CYTOTOXIC AGENTS
FILE REFERENCE: 142184WO
CURRENT APPLICATION NUMBER: US/10/240,198
CURRENT PILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 0009887.1
PRIOR APPLICATION NUMBER: 0009887.1
PRIOR APPLICATION NUMBER: 0009887.1
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATCHILIN VET: 2.1
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LOCATION: (94)
COTHER INFORMATION: Unpaired base
15-10-240-198-2
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NAME/KEY: misc_feature
LOCATION: (72)
OTHER INFORMATION: Unpaired base
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Best Local Similarity 100.
Matches 125; Conservative
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OTHER INFORMATION: ITR
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US-09-782-378A-6
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LENGTH: 145
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US-10-054-665-7
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                                                                                                                                                                                                                                                        Query Match
100.0%; Score 125; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 125; Conservative 0; Mismatches 0; Indels
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; Publication No. US20020197237A1
; GENERAL INFORMATION:
APPLICANT: Engelhardt, John F.
; APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
; FILE REFERENCE 875.007US2
; CURRENT APPLICATION NUMBER: US/10/054,665
; CURRENT PILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/276,625
; PRIOR APPLICATION NUMBER: US 00/086,166
; PRIOR FILING DATE: 1999-03-25
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030152914A1
GENERAL INFORMATION:
APPLICANT: Kaplitt, Michael G.
APPLICANT: Musacov, Serge
TITLE OF INVENTION: Method for Generating Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Best Local Similarity 100.
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTGGCCACTCCCT
; SEQ ID NO 6
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-378A-8
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ORGANISM: Unknown
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US-10-159-968-13/c
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; FEATURE:
; OTHER INFORMATION: Inverted terminal repeat from the AAV-2 vector plasmid pSub 201
US-10-276-356-1
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## Publication No. US20040029106A1

## Publication No. US20040029106A1

## Publicant: University of No. US20040029106A1th Carolina at Chapel Hill

## PELICANT: University of No. US20040029106A1th Carolina at Chapel Hill

## APPLICANT: Samulski, R. Jude

## APPLICANT: MCALTY, Douglas M.

## TITLE OF INVENTION: DUPLEEED PREVOVIRUS VECTORS

## TITLE OF INVENTION: UNDERED PREVOVIRUS VECTORS

## CURRENT FILING DATE: 2001-05-31

## PRIOR PELING DATE: 2001-05-31

## NUMBER OF SEQ ID NOS: 1

## SOFTWARE: Patentin Version 3.1

## SEQ ID NO: 1

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TITLE OF INVENTION: Defective Viral Vectors That are Helper Free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 125; DB 14; Length 165; Best Local Similarity 100.0%; Pred. No. 1.3e-25; Matches 125; Conservative 0; Mismatches 0; Indels 0
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                                    FILE REFERENCE: 600-1-286
CURRENT APPLICATION NUMBER: US/10/159,968
CURRENT APPLICATION NUMBER: US/02-05-31
PRIOR APPLICATION NUMBER: US 60/294,797
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRCANISM: Adeno-associated virus
US-10-159-968-13
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; ORGANISM: Homo sapiens
US-09-845-416-33
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-845-416-26
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LENGTH: 955
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Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICANT: XAPO

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT APPLICATION NUMBER: 02001-04-30

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SSOTHARE: Patentin Ver. 2.1

SSOTHARE: Patentin Ver. 2.1

SSOTHARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: synthetic enzyme attachment site sequence
US-10-023-208-58
                         Sequence 58, Application US/10023208

Publication No. US20030124537A1

GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Win Ching
TITLE OF INVENTION: PROCARYOTIC LIBEARIES AND USES
FILE REFERENCE: A-70174-1/RFT/RMS/RNK
CURRENT APPLICATION NUMBER: US/10/023,208
CURRENT PILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/256,163
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 125; Conservative
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Best Local Similarity 100.
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-845-416-26
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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US-09-845-416-26
                 15-10-023-208-58
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LENGTH: 207
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Sequence 33. Application US/09845416

Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICANT XIAO, XIAO

TILLE OF INVENTION: THERBOF

TILLE REFERENCE: DE1142

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT PILLING DATE: 2001-04-30

PRIOR FILLING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LUNGTH: 987
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US-09-845-416-26/c

Sequence 26, Application US/09845416

Sequence 26, Application US/09845416

Sequence 26, Application US/09845416

SENERAL INFORMATION:
TITLE OF INVENTION: DAS SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/200,777

PRIOR APPLICATION NUMBER: 60/200,777

SOFTWARE PATENTING OF 22

SOFTWARE PATENTING US: 36
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100.0%; Score 125; DB 10;
Best Local Similarity 100.0%; Pred. No. 8.8e-26;
Matches 125; Conservative 0; Mismatches 0;
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| Publication No. US20030171312A1
| GENERAL INFORMATION |
| APPLICANT: XIAO, XIAO
| TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE |
| TITLE OF INVENTION: THEREOF |
| TITLE OF INVENTION: DATE: 2001-04-30 |
| PRIOR PILLING DATE: 2001-04-28 |
| NUMBER OF SEQ ID NOS: 36 |
| SOFTWARE: Patentin Ver. 2.1 |
| LENGTH: 4414
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-845-416-33/c

| Sequence 313 / Application US/09845416
| Publication No. US20030171312A1
| Fublication No. US20030171312A1
| GENERAL INFORMATION:
| APPLICAMT IND.
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: DE1142
| FILE REFERENCE: DE1142
| CURRENT FILING DATE: 2001-04-30
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 36
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 987
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CRGANISM: Homo sapiens
US-09-845-416-32
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ORGANISM: Homo sapiens
US-09-845-416-33
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US-09-845-416-32
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US-09-845-416-32/c
US-09-845-416-32/c
| US-09-845-416-32/c
| Sequence 32, Application US/09845416
| Publication No. US20030171312A1
| GENERAL INFORMATION:
| APPLICANT: XIAO, XIAO, XIAO
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: US/09/845,416
| CURRENT APPLICATION NUMBER: US/09/845,416
| PRIOR PELLING DATE: 2001-04-30
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 36
| SOFTHARE: ParentIn Ver. 2.1
| SEQ ID NO 32
| USANTHE OF SET OF THE OF THE
1 TTGGCCACTCCCTCTTGGGGGCTCGCTCGCTCAAAGGCCGAGCCGAAGGTCGCC 60
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Matches 125; Conservative
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ORGANISM: Homo sapiens
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Sequence:

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| Sequence 1, Application Us/07789917A |
| Patent No. 5252479 |
| GENERAL INFORMATION: |
| APPLICAMY: Srivateva, Arun |
| STATE: OF INSTITUTE |
| STATE: OF INSTITUTE |
| STATE: New York |
| CONFURE: Soully, Scott, Murphy Presser |
| CONFURE: New York |
| CONFURE: New York |
| CONFURE: Eloppy disk |
| CONFURE: Readable Form: |
| MEDIUM TYPE: Floppy disk |
| CONFURE: Patentin Release q.0, Version q.25 |
| SOFTWARE: Patentin Release q.0, Version q.25 |
| SOFTWARE: Patentin Release q.0, Version q.25 |
| CONFURE: Patentin Release q.0, Version q.25 |
| SOFTWARE: Patentin NUMBER: US/07/789,917A |
| FILING DATE: 19911118 |
| FILING DATE: 19911118 |
| FILING DATE: 19911118 |
| FELECOMMUNICATION NUMBER: 22,606 |
| REPERATION NUMBER: 23,666 |
| REGISTRATION NUMBER: B361 |
| TELEFAM: (516) 742-4343 |
| TELEFAM: (516) 742-4346 |
| TELEFAM: (516) 742-4346
                                                                                  US-09-299-141-17
US-09-299-141-7
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US-09-299-141-3
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US-09-299-141-5
US-09-276-625-4
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US-07-789-917A-1
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Matches 145;
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US-07-789-917A-1
   Query Match
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Sequence 9,
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145
1 TIGGCCACICCCTCTGGG.......CTCCATCACTAGGGGTTCCT 145
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1: /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-440-194-1
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US-08-276-625-1
US-08-29-19-1
US-09-29-141-4
US-09-299-141-8
US-09-299-141-8
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US-08-893-327-15
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Listing first 45 summaries
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APPLICANT: DENEFLE, Patrice
APPLICANT: DENEFLE, Patrice
APPLICANT: DENEFLE, Emmanuelle
APPLICANT: VIGNE, Emmanuelle
APPLICANT: NYENEL EMMANUELE
APPLICANT: PRENICAUEL, MITEGRATIVE RECOMBINANT ADENOVIRUSES,
TITLE OF INVENTION: PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
Gaps
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Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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LOCATION: 1...145
OTHER INFORMATION: /note= "Minimal ITR Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
FILING DATE:
CLASSIFICATION: 424

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/02445

FILING DATE: 03-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00233

FILING DATE: 28-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619

REFERENCE/DOCKET NUMBER: 38,619

REFERENCE/DOCKET NUMBER: 38,619

TELEPHONE: (610) 454-3839

TELEPHONE: (610) 454-3839

TELEPHONE: (610) 454-3808

INFORMATION FOR EGO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs

TYPE: nulleic acid
STANDEDUSS: double

TOPPOLOGY: linear

MOLECULE TYPE: other nucleic acid
                                                               121 GCCAACTCCATCACTAGGGGTTCCT 145
                                                                                                     121 GCCAACTCCATCACTAGGGGTTCCT 145
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US-08-702-573-4
; Sequence 4, Application US/08702573
; Patent No. 6033885
; GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,193
FILING DATE: 19921125
CLLSSIFICATION: 435
ATCARSIFICATION: William E.
REGISTRATION NUMBER: 22,606
REFERENCH: (516) 742-433
TELECOMUNICATION NUMBER: 8361
TELEFACE (516) 742-4366
TELEFACE
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APPLICANT: Samulski, R. J.
APPLICANT: X.
APPLICANT: X.
TITLE OF INVENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                       US-07-982-193-1

| Sequence 1, Application US/07982193
| Patent No. 6261834
| GENERAL INFORMATION:
| APPLICANT: Stivastava, Arun
| TITLE OF INVENTION: SAPE VECTOR FOR GENE THERAPY
| TITLE OF INVENTION: 2APE VECTOR FOR GENE THERAPY
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS: 
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TYPE: NUCLEIC ACID
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CITY: Garden City
STATE: New York
COUNTRY: USA
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Best Local Similarity
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US-07-989-841A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 145; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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100.0%; Score 145; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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Patent No. 6657152
GENERAL INFORMATION:
APPLICANT: Samulski, R.
APPLICANT: Samulski, R.
APPLICANT: Samulski, R.
APPLICANT: Samulski, R.
CURRENT ENFERRENCE: 6636-027
CURRENT PILION DATE: 1995-06-06
CURRENT FILING DATE: 1995-06-15
CURRENT PILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GCCAACTCCATCACTAGGGGTTCCT 145
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                                                                                                                                                6636-022
FILING DATE: May 15, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6636-0
TELEPANE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-440-738A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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US-08-471-914-1
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APPLICANT: Samulski, R. J.
APPLICANT: Recombinant Viral Vector System
NUMBER OF SEQUENCES:
ADDRESSE: Pennie & Edmonds
STRET: 1155 Avenue of the Americas
CITY: New York
CUTY: New York
CUTY: New York
COMPUTER: 1155 Avenue of the Americas
APPLICATION TYPE: FOPPY disk
COMPUTER: 18P FC compatible
COMPATICATION NUMBER: US/08/440,738A
                                         ADDRESSEE: Pennie & Edmonds
CITY: New York
STATE: New York
CUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN FC COMPATIBLE
OMPUTER: PATENTIN PC-DOS/NS-DOS
SOFTWARE: BATENTIN PR-BATENTIN PR-BATENTIN PATE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,841A
FILING DATE: On even date herewith
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COPILET, US/089,841A
FILING DATE: On even date herewith
CLASSIFCATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6636-013
TELECOMMONICATION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: 6641 PENNE
TELEFAX: 665 DASE PATE
THOORNATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 DASE PATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DB 1;
4.3e-31;
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Best Local Similarity 100.0%; Pred. No. 4
Matches 145; Conservative 0; Mismatche
                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GCCAACTCCATCACTAGGGGTTCCT 145
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Patent No. 5869305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-440-738A-1
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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NAME: NO. 5766211and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 31975
TELEPOWINICATION INFORMATION:
TELEPHONE: (312) 474-6448
TELEPRA: 25-3656
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE FARRACTESISTICS:
SEQUENCE FARRACTESISTICS:
TELECOMMUNICATION INFORMATION:
TELEBEAX: (312) 474-6300
TELEFAX: (312) 474-0448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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STRANDEDNESS:
TOPOLOGY: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-475-391-1
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) OTHER INFORMATION: SEQ ID NO:1 of U.S. Patent No. 6436392 5,478,745
US-09-276-625-7
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Jeduence 1, Adeno-Associated Virus Materials and TITLE OF INVENTION: Methods

JUNER OF SEQUENCES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: G300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois

COUNTRY: USA

ZIP: G0606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Datentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE:

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 145; DB 4; Length 165; Best Local Similarity 100.0%; Pred. No. 4.3e-31; Matches 145; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                 APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.007031
CURRENT FILING DATE: 1999-03-25
CURRENT FILING DATE: 1999-03-25
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 165
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141 GCCAACTCCATCACTAGGGGTTCCT 165
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658785and, Greta E.
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
                                                                                                                                                                               US-09-276-625-7; Sequence 7, Application US/09276625; Patent No. 6436392; ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown
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US-08-254-358-1
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PATCHE NO. 5786211

GENERAL INPORMATION:
ITILE OF INVENTION: Adeno-Associated Virus Materials and TITLE OF INVENTION: Methods
ITILE OF INVENTION: Methods
INVERSE ONDERSES:
ADDRESSES:
ANDRESSES:
ADDRESSES:
ANDRESSES:
AND
Query Match
100.0%; Score 145; DB 1; Length 4680;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 145; Conservative 0; Mismatches 0; Indels 0
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RESULT 11
PCT-US95-07178-1
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1. Application US/08709609
| Sequence 1. Application US/08709609
| Patent No. 5858775
| GENERAL INFORMATION:
| APPLICANT: Johnson, Philip R. TITLE OF INVENTION: Methods
| TITLE OF INVENTION: Methods | ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
| COUNTRY: USA | COMPUTE: Illinois COMPUTE: Illinois COMPUTE: Illinois COMPUTE: Patentin Release #1.0, Version #1.25
| COMPUTE: Patentin Release #1.0, Version #1.25
| CURRENT APPLICATION NUMBER: US/08/709,609
| FILING DATE: Patentin Release #1.0, Version #1.25
| CLASSIFICATION NUMBER: 35,302
| RETERENCE/DOCKET NUMBER: 35,302
| RELEPHONE: (312) 474-6300
| TELEPHONE: (312) 474-6448
| TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6468
| TELEPHONE: LENGTH HARDATERISTICS: LENGTH: 46A0 hae naive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4680;
                                 100.0%; Score 145; DB 1; Length 4680; 100.0%; Pred. No. 5.8e-31; ive 0; Mismatches 0; Indels 0
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100.0%; Score 145; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 145; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                               Query Match
Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           US-08-709-609-1
US-08-475-391-1
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1 TIGGCCACTCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACGAAAGGTCGCC
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                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9507178

Sequence 1, Application PC/TUS9507178

GENERAL INPORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago
STATE: 111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4680;
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Sequence 4, Application US/09299141

PRECENT NO 6461606

GENERAL INFORMATION:

APPLICANT: FLOTTE, TERENCE R.

APPLICANT: SONG, SIHONG

APPLICANT: BYRNE, BARRY J.

APPLICANT: MORAN, MICHAEL

TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60660
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07178
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGERT INFORMATION:
NAME: Noland, Greta 85,302
REFREENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TOWNAMEN: 31975
TELECOMMUNICATION TOWNAMEN: 31075
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100.0%; Score 145; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 145; Conservative 0; Mismatches 0;
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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                                                    US-09-299-141-8
; Sequence 8, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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100.0%; Score 145; DB 4; Length 5932;
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 145; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                     ; FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:p43C-AT
US-09-299-141-4
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OTHER INFORMATION: Description of Artificial Sequence:p43C-AT
US-09-299-141-4
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US-09-299-141-4/C
Sequence 4, Application US/09299141
Sequence 8, Application US/09299141
Patent No. 6461606
GENERAL INFORMATION:
APPLICANT: FLOTTE, TERRNCE R.
APPLICANT: SONG, SIHONG
APPLICANT: MORGAN, MICHAEL
TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REPERENCE: 4300-011800
CURRENT APPLICATION NUMBER: US/09/299,141
CURRENT FILING DATE: 1999-04-23
BARLIER APPLICATION NUMBER: 60/083,025
BARLIER PILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 5932
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100.0%; Score 145; DB 4; Length 59
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: 4300.011800
CURRENT APPLIACATION NUMBER: US/09/299,141
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/083,025
BARLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
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LENGTH: 5932
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APPLICANT: SONG, SIHONG
APPLICANT: SONG, SIHONG
APPLICANT: BARRA, BARRA
APPLICANT: BARRA, BARRA
APPLICANT: BARRA, BARRA
APPLICANT: BARRA
APPLICANT: BARRA
TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REFREATOR
CURRENT APPLICATION NUMBER: US/09/299,141
CURRENT FILING DATE: 1999-04-23
CURRENT FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 8
SEQ ID NO 8
LENGTH: GA42
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| Sequence 8, Application US/09299141
| Sequence 8, Application US/09299141
| Patent No. 6461606
| GENERAL INFORMATION:
| APPLICANT: FLOTTE, TERENCE R.
| APPLICANT: SONG, SIHONG
| APPLICANT: BYRNE, BARRY J.
| TITLE OF INVANTION: MATERIALS AND METHODS FOR GENE THERAPY
| TITLE OF INVANTION: MATERIALS AND METHODS FOR GENE THERAPY
| FILE REFERENCE: 4300.011800
| CURRENT FILING DATE: 1999-04-23
| EARLIER PPLICATION NUMBER: 60/083,025
| BARLIER PLING DATE: 1999-04-24
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 8
| LENGTH: 6142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 145; DB 4; Length 61
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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1 TTGGCCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60 a & a ઠે

Search completed: April 1, 2004, 17:04:17 Job time: 65.7593 secs

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April 1, 2004, 12:58:58; Search time 243.815 Seconds (without alignments) 2526.461 Million cell updates/sec
                                                                                                                                                                                         US-10-620-039-1
145
1 TTGGCCACTCCCTCTCTGCG.......CTCCATCACTAGGGGTTCCT 145
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                   3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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1: geneseqn1980s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

lon	AAV2 inve Strict in Adeno-ass	Human ade Adeno ass AAV-2 lef	Adeno-ass Double-D Adeno ass Inverted	Human ade Nucleotid 165 bp en Adeno-ass Adeno-ass Adeno-ass	Adeno-ass Adeno-ass Adeno-ass Adeno-ass Adeno-ass Adeno-ass
Description	Aaq41448 Aat03385 Aax34295	Abs69884 Acc58491 Acf35876	Abx93568 Aaq66769 Aat49462 Aad03535	Abs69886 Abv77279 Aad44621 Aad37254 Aad37254	Add37261 Add37260 Add37260 Add37259 Add37259 Add37258
	a.				
SUMMARIES	AAQ41448 AAT03385 AAX34295	ABS69884 ACC58491 ACR35876	ABX93568 AAQ66769 AAT49462 AAD03535	ABS69886 ABV77279 AAD44621 AAD37254 AAD37254	AAD37261 AAD37260 AAD37260 AAD37259 AAD37259 AAD37258
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Score	145 145 145	1111 1441 1455	11 11 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15	u i u u u u 4 4 4 4 4 4 0 0 0 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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	Aaf89931 Nucleotid	Aba02989 Adeno-ass	Abs69879 Human ade	Abs69880 Human ade	-		-	-	Abv76133 Adeno ass	Aat09008 Wild-type		Ada50070 Adeno-ass	Ade81075 Adeno-ass			Aad37257 Adeno-ass	Aad37263 Adeno-ass	Aad37256 Adeno-ass	. Aad37256 Adeno-ass	Aad37262 Adeno-ass	Aad37262 Adeno-ass
5 4 AAH41481	S 4 AAF89931	5 6 ABA02989	5 6 ABS69879	5 6 ABS69880	o,	9 4 AAI66974	9 4 AAF23750	v	9 7 ABV76133	71	7	œ	0 9 ADE81075	4	5 6 AAD37257	5 6 AAD37257	8 6 AAD37263	6 6 AAD37256	6 6 AAD37256	0 6 AAD37262	0 6 AAD37262
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24 1	25 1	26 1	27 1	28	29 1	30	31	32 1	33	34 1	35 1	36 1	37 1	38	39	c 40	C 41 1	42	G 43	44	c 45 1

ALIGNMENTS

SUL 241	T 1 448 AAQ41448 standard;	lard; DNA; 145 BP.
	AAQ41448;	
	25-MAR-2003 (27-AUG-1993 (revised) (first entry)
•	AAV2 inverted	terminal repeat.
	Adeno-associated virus cell-specific; gene the sickle cell anaemia; ca	Adeno-associated virus 2; ITR; site-specific integration; vector; cell-specific; gene therapy; haemoglobinopathies; thalassemia; diabetes; sickle cell anaemia; cancer; parvovirus; B19; ss.
	Adeno-associated virus	ed virus 2.
XX FH Key FT rep FT	Key repeat_region	Location/Qualifiers 1125 /*tag= a /note= "inverted terminal repeat forming palindromic hairnin"
	misc_feature	42. 83 /*tag= b /note= "Flip orientation"
	WO9309239-A1.	
	13-MAY-1993.	
	06-NOV-1992;	92WO-US009769.
	08-NOV-1991;	91US-00789917.
	(RESE) RESEAR	RESEARCH CORP TECHNOLOGIES INC.
PI Sr	Srivastava A;	
	WPI; 1993-167704/20	704/20.
PT Ade PT of	Adeno-associated virus-2 of haemoglobinopathies ar capable of cell-specific of the adeno-associated v	Adeno-associated virus-2 basal vectors - for gene therapy and treatment of haemoglobinopathies and cancer etc has cassette contg. a promoter capable of cell-specific expression, between 2 inverted terminal repeats of the adeno-associated virus 2.
	Disclosure, Fi	Fig 1; 68pp; English.

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The sequence is one of two inverted terminal repeat sequences, one from parvovirus B19 and the other from adeno-associated virus 2 (AVV2), used in construction of an expression vector for site specific integration and cell specific gene expression. The vector comprises at least one cassette conty: a promoter capable of effecting cell-specific expression, operably linked to a hetero-logous gene, and the cassette residing between the inverted terminal repeats. The vector is safe for use in gene therapy, partic. In treatment of haemoglobinopathies and a variety of diseases, e.g. thalassemia, diabetes, sickle cell anaemia, and cancer. See also AAQ41449. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant, non-pathogenic adenovirus which are able to integrate stably into a host genome are claimed. The viruses pref. contain at least one inverted terminal repeat (TTR) sequence and in particular two TTRs flank a heterologous DNA insert. The present sequence is that of the strict TTR from adeno associated virus AAV-2 (i.e. the ITR sequence without any deletions or additions). In the construct pITRFL, the beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                       inverted terminal repeat, ITR, adenovirus, adeno-associated virus, AAV-2, replication defective, integration, gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                   1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant defective adenovirus contg. integratable expression cassette - for use in gene therapy to express protein, antigen or anti:sense nucleic acid, also for prodn. of recombinant adeno-associated viruses.
                                                                                                                                                                                                                                                                                                                                               1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                Query Match 100.0%; Score 145; DB 2; Length 145; Best Local Similarity 100.0%; Pred. No. 8.1e-30; Matches 145; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strict inverted terminal repeat from AAV-2, used in pITRFL.
                                                                                                                                                                                                                               Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
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(first entry)
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18-APR-1996
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marker gene is flanked by two strict AAV-2 ITRs. The defective viruses are useful for stably introducing large fragments of heterologous DNA making them suitable for gene therapy. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                              1 TTGGCCACTCCCTCTGTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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                                                                                                                                                                                                                                                                                                            Gaps
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promoter; rep; cap; inverted terminal repeat; ITR; erythroid cell
integration; gene expression; bone marrow; peripheral blood cell;
endothelial cell; myocardial cell; ss.
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                                                                                                                                                                                                                                             Length 145;
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                                                                                                                                                                              49 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          100.0%; Score 145; DB 2;
100.0%; Pred. No. 8.1e-30;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                              Sequence 145 BP; 21 A; 52 C;
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Best Local Similarity 100.0
Matches 145, Conservative
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AAX34295
ID A4X34295
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Length

DB 2;

100.0%; Score 145;

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                                                                                                                                                                                                                                                                                                                                                          Vector; adenovirus; adeno-associated; adenosine deaminase gene; recepted adenoine deaminase deficiency; severe combined immune deficiency; PAH, beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylketonuria; dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antilipaemic; noctropic; cytostatic; dermatological; human adeno-associated virus 2; AAV2; terminal repeat; ds
                                         1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGAAGGTCGCC
                                                                                              Gaps
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              Indels
                                                                                                                                                                                                                                                                                                                                   Human adeno-associated virus 2 terminal repeat sequence.
100.0%; Pred. No. 8.1e-30; ive 0; Mismatches 0;
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                                                                                                                                                                       GCCAACTCCATCACTAGGGGTTCCT
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Best Local Similarity 100.
Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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disease, receptor for low density lipoprotein gene associated with familial hypercholesterolaemia, hypoxanthine-guanine phosphorizansferase associated with leach-Wyhan syndrome, phosphorizansferase associated with leach-Wyhan syndrome, dystrophin gene associated with muscular dystrophy, and human cystic fibrosis transmembrane conductance regulator gene associated with cystic fibrosis. The present nucleic acid sequence represents a human adenoses sociated virus 2 (AAV2) terminal repeat sequence that was used in the methods of the invention
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                                                                                                                                                                                                                                                                                 Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
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100.0%; Pred. No. 8.1e-30;
iive 0; Mismatches 0;
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21. .145
/*tag= a
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13-AUG-2002; 2002US-00216870.
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ID ACC58491 standard; DNA; 145
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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The invention relates to a recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed. A complete vitus-mediated system for recombinant AAV production is provided which comprises: (a) a first recombinant adenovirus encoding one or more AAV REP78/68 polypeptides and one or more viral capsid polypeptides; (b) a second recombinant adenovirus comprising a gene of interest and AAV inverted terminal repeats that flank the gene of interest; (c) viral helper functions; and (d) a host cell comprising the first recombinant adenovirus, the second recombinant adenovirus, and the viral helper functions. The recombinant AAV is useful as a vector for gene therapy. The present sequence represents an AAV-2 left inverted terminal repeat (ITR) sequence
ITR and coding sequences for AAV VP1, VP2 and VP3 capsid proteins, for AAV non-structural replication (Rep) proteins Rep52 or Rep40, and for AAV Rep78 or Rep68. The method of producing AAV in insect cells provides an efficient, safe and economical means of producing a large amount of recombinant AAV particles which may be used in gene therapy
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                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 145; DB 7; Length
Best Local Similarity 100.0%; Pred. No. 8.1e-30;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                Sequence 145 BP; 23 A; 49 C; 52 G; 21 T; 0 U; 0 Other;
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ACF 3876

ACF 38
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Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;

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/+tag= molety= "Nucleotides 125-85 of the present
sequence"
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/*tag= b
/bound_moiety= "Nucleotides 62-54 of the present
sequence"
54. 62
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/bound_molety= "Nucleotides 72-64 of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotides 84-76 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /bound moiety= "Nucleotides 41-1 of 93...1\overline{0}8
                                                                                                                                                                                                                        Adeno-associated virus-2 inverted terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= g
/label= Rep recognition sequence
/note= "This RRS is specifically
/*:
100.0%; Score 145; DB 8;
100.0%; Pred. No. 8.1e-30;
ive 0; Mismatches 0;
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/label= Terminal_resolution_site
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                                                                                                         121 GCCAACTCCATCACTAGGGGTTCCT 145
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                         121 GCCAACTCCATCACTAGGGGTTCCT
                                                                                                                                                                                                                                                                   Adeno-associated virus serotype 2.
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                                                                                                                                                                    ABX93568 standard; DNA; 146
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85. .125
          11 Similarity 100.
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Matches 145
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                                                                                                                                                                                   The invention relates to identifying molecules that interact with an adeno-associated viral regulatory element (e.g.a Rep recognition sequence, RRS) comprising contacting at least one molecule with a nucleic sequence, RRS) comprising on adeno-associated viral regulatory element, and identifying whether at least one molecule is bound to the viral requiatory element. Also included is a kit for analysing the interaction between molecules and an adeno-associated viral regulatory element. The method is useful for identifying molecules e.g. at least one cellular protein, synthetic protein or exogenous protein proteins that are derived from a cDNA library or cellular lysate), or peptide, antibody, nucleic acid, lipid, carbohydrate and/or organic or inorganic compound that interacts with an adeno-associated viral regulatory element comprising an inverted terminal repeat (ITR) or region. The method broadens the understanding of adeno-associated virus (AAV) and facilitates the application of adeno-associated virus-based vector system, therefore ITR-binding proteins and other molecules provide new insights into the AAV life cycle, including the requiation of game expression and integration, and suggestes improvements for its application in therapy. The present est an
                                                                                                                    contacting an adeno-associated viral regulatory interacting molecule with a nucleic acid comprising a adeno-associated viral regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of cellular regulations of adeno-associated virus involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Double-D ITR; inverted terminal repeat; D-sequence; AAV; adeno-associated virus; capsid; encapsidation; gene therapy; vector; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 146 BP; 21 A; 53 C; 49 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                             Disclosure, Fig 1; 16pp, English.
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                                            Cathomen AJ;
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(first entry)
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Best Local Similarity 100.
Matches 145; Conservative
(WEIT/) WEITZMAN M D. (CATH/) CATHOMEN A J.
                                                                      WPI; 2003-328607/31
                                            Weitzman MD,
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20-JAN-1995
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/*tag= m
/label= Double-D
a note= "Touble 165 bp sequence, resulting from addition of
a second D rispeat to the AAV ITR, has not been identified
in any naturally occurring virus"
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/standard_name= "ITR"
/note= "This naturally occurring 145 bp ITR is located at both ends of the AAV genome"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TIGGCCACICCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenovirus associated viral inverted terminal repeat - for use in recombinant viral vector system for treatment of genetic diseases
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93WO-US011728.
                                                                                     92US-00989841
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                                                                                                                          gene sequences remain intact
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(ENGE/) ENGELHARDT J F.
(DONG/) DONGSHENG D.
(ZIYI/) ZIYING Y.
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/label= T-shaped
/note= The naturally occurring 145 bp ITR sequence can
form a T-shaped structure for DNA replication when single
                                                                                                       /rpt_type= INVERTED
/labol= A' repeat
/note= "forms the stem of a T-shaped structure when base
paired with repeat A"
                                                                                                                                                                                                                                                                                                                                                                                                of a T-shaped structure when base
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                                                                                                                                                                                                                                                           /*tag= k
/note= "Part of T-shaped structure, formed by base
pairing between the B' and B repeats"
85. 92
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//*tag= part of T-shaped structure, formed by base
pairing between the C' and C repeats"
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Additional D' sequence"
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/label= A repeat
/note= "Forms the stem
paired with A' repeat"
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/label= C_repeat
84. .104
                /rpt_type= INVERTED
/label= D_repeat
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label= C'_repeat
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|label= B_repeat
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                                     misc_structure
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(ITR) located at each end of its genome. In addition to being able to base pair with each other, the ITRs can also individually fold back on themselves through the base pairing of A, A', B, B, and C, C' sequences to form a T-shaped structure for DNA replication (see features table). It has been found that viral mutants with deleted D sequences are unable to replicate their DNA. Addition of second D repeat (D') to the naturally occurring ITR resulted in a sequence, designated double-D, which was sufficient to carry out the functions normally required of two wild-type ITRS during a lytic AAV viral infection, i.e. it is capable of directing replication and assembly into AAV, and/or the integration into the host genome, of recombinant DNA containing the nucleic acid molecule. Vectors and viral particles containing the double-D sequence are useful in gene therapy. Replication and integration into the host genome is completely effected through the double-D sequences, ensuring that the heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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100.0%; Score 145; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.2e-30;
Matches 145; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GCCAACTCCATCACTAGGGGTTCCT 145
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01-AUG-2002.

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The patent discloses a composition comprising at least two recombinant adeno-associated viruses (rAAVs). Each rAAV contains a recombinant DNA molecule comprising three DNA segments linked together. The first and the third DNA segments of inverted terminal repeats (ITRs) respectively from the circular intermediate of AAV. The second DNA segment in each virus is different and does not comprise AAV sequence. It preferably comprises sequences sequences or comprise AAV sequence. It profession (PPR), the erythropoietin (Epp) gene, the tyrosine hydroxylase gene (Parkinson's syndrome) or the glucocare- brosidase gene (Parkinson's syndrome) or the glucocare- brosidase gene (Parkinson's syndrome) or the glucocare- brosidase gene (Gaucher's disease). The circular intermediate of AAV imparts increased episomal stability and persistence of the vector in the host cell. Compositions comprising rAAV sequences are useful for transferring recombinant DNAs to a host cell and express a polypeptide in a host cell and expresses are useful for transferring recombinant vector is useful in medical therapy, which includes the amendant propositions of disease, muscle disorders involving skeletal, cardiac or smooth muscle. AAV vector is used as a delivery vehicle for a sequence is the ITR DD DNA sequence referred to as "double sequence". This sequence is the ITR DD DNA sequence referred to se "double sequence". This sequence is the present invention
Composition for transferring recombinant DNAs and to express a polypeptide in a host cell, comprises two recombinant adeno-associated viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                        Disclosure, Page 139; 144pp; English.
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                                                                                                          TIGGCCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCCGACCAAAGGTCGCC 80
                                                                             1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                           Gaps
Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-30;
Matches 145; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                        GCCAACTCCATCACTAGGGGTTCCT 145
                                                                                                                                                                                                                                                 141 GCCAACTCCATCACTAGGGGTTCCT 165
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Human adeno-associated virus 2 terminal repeat DD sequence.
    ABS69886 standard; DNA; 165 BP.
                      21-NOV-2002 (first entry)
ABS69886
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Vector; adenovirus; adeno-associated; adenosine deaminase gene; recepto adenosine deaminase deficiency; severe combined immune deficiency; PAH; beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; hypoxanthine-guanine phosphoribosyltransferase; lesch-Nyhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylketomuria; dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antilipaemic; nootropic; cytostatic; dermatological; human adeno-associated virus 2; AAV2; terminal repeat; ds.

Homo sapiens

US2002102731-A1

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The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (NS) having 5' and, left and right inverted terminal repeats of adenovirus packaging sequence linked to inverted terminal repeats of terminal repeats of adenovirus packaging sequence linked to inverted terminal repeat flanked to 3' end of NS, into cell expressing adenovirus early gane lacking from vector of and culturing cell to produce another vector. The method is useful in transferring nucleotide sequences of interest into a cell, for gene transferring nucleotide sequences of interest into a cell, for gene transferring nucleotide sequences are useful for treating diseases associated with it, i.e. adenosine deaminase gene associated with adenosine deaminase cell, for transferring into second this severe combined immune deficiency, beta-chain of the memoglobin gene associated with beta-thalassaemia and sickle cell disease, receptor for low density lipoprotein gene associated with syntamine hydroxylase (PAH) gene associated with phenylketonuria, construction of the phosphoribosyltransferase associated with ineschance in the phosphoribosyltransferase associated with heach-Nyhan syndrome, construction gene associated with mescular dystrophy, and human cystic fibrosis transmembrane conductance regulator gene associated with expresents a human adenoment of associated virus 2 (AAVVZ) terminal repeat sequence that was used in the
                                                                                                                                                                                                                                                                                                                       adenovirus inverted terminal repeats and packaging sequence, and adeno-
associated virus terminal repeat, into cell, and culturing cell.
                                                                                                                                                                                                                                                                                                  Producing vector, by introducing vector having nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 165 BP; 24 A; 59 C; 53 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                  Gnatenko DV;
                                                                                                                                                  (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                  Sandalon Z,
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 8; 191pp; English.
                                                                                                  02-OCT-2000; 2000US-0237747P.
                                                  12-FEB-2001; 2001US-0078237B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methods of the invention
                                                                                                                                                                                                  Bahou WF,
                                                                                                                                                                                                                                                    WPI; 2002-690619/74.
                                                                                                                                                                                                    Hearing P,
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ö 9 80 1 Indecendence Terreses and Ter 21 rrescencrecerereses de contractor de la resecue de contractor de cont 0; Gaps Query Match 100.0%; Score 145; DB 6; Length 165; Best Local Similarity 100.0%; Pred. No. 8.2e-30; Matches 145; Conservative 0; Mismatches 0; Indels 121 GCCAACTCCATCACTAGGGGTTCCT 145 셤 ઠે g ò ઠ

Nucleotide sequence of pTRT, a circular adeno-associated virus. Circular adeno-associated virus; cAAV; replication; hairpin; gene therapy; pTRT; ss. 141 GCCAACTCCATCACTAGGGGTTCCT 165 ABV77279 standard; DNA; 165 28-MAR-2003 (first entry) ABV77279; RESULT 12 g

14-DEC-2001; 2001WO-US049058

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31-MAY-2001; 2001US-0294797P.
07-AUG-2001; 2001US-0313007P.
                                31-MAY-2002; 2002WO-US017324
                                                                Kaplitt MG, Moussatov S;
                                                      (UYRQ ) UNIV ROCKEFELLER
    Adeno associated virus
                                                                          WPI; 2003-103706/09
             WO200297056-A2
                      05-DEC-2002,
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The specification describes a nucleotide sequence capable of directing circular adeno-associated virus (CAAV) replication. This nucleotide sequence comprises a loop sequence (TGGCAAA) finhwed on the 5' and 3' sides by complementary sequences, where a hairpin structure is formed between the complementary sequences. The CAAVs are useful in gene therapy, e.g. to treat an acute medical condition a nucleic acid encoding a therapeutic protein is inserted into the cAAV. The present sequence represents pTRT, a cAAV that contains a wild-type dircularization point (the TRT domain), consisting of a single ITR flanked by two D-sequences Production of defective viral vectors for gene therapy that are completely free of helper viral vectors and helper viruses. Length 165; Seguence 165 BP; 26 A; 56 C; 56 G; 27 T; 0 U; 0 Other; Example 4; Page 53; 69pp; English

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9
                                                                     145 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGGGACAAAGGTCGCC 86
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                                                                                                                            1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGCGACCAAAGGTCGCC
                            Gaps
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                            0; Indels
Query Match
100.0%; Score 145; DB 7;
Best Local Similarity 100.0%; Pred. No. 8.2e-30;
Matches 145; Conservative 0; Mismatches 0;
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101

AAD44621 standard; DNA; 207 (first entry) 13-DEC-2002 AAD44621; RESULT 13

ВР

165 bp enzyme attachment site (EAS) DNA.

Prokaryotic library; candidate protein; nucleic acid modification; NAM; enzyme attachment sequence; EAS; clinical pharmacology; chemical sensor; enzymology; cosmetic research; toxic; environmental safety assessment; nutrient blology; enzyme attachment site; EAS; ds.

Unidentified

WO200266653-A2

29-AUG-2002

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The invention relates to methods and compositions for the construction of prokaryotic libraries expressing candidate proteins and the use of these libraries to identify candidate proteins and the nucleic acids encoding them. The invention provides a library of prokaryotic pET-24a vectors comprising a fusion nucleic acid consisting of anucleic acid encoding a constraint of a constitute of a candidate protein, or the candidate protein, or an encoding these proteins; in screening for NAM enzyme the candidate proteins and an enzyme attachment sequence (EAS) recognised by the NAM enzyme. The library is used for identifying candidate proteins and uncleic acids encoding these proteins, or in identifying novel or improved EASs, which may be used for understanding cellular processes or improved EASs, which may be used for understanding cellular processes or any subsequent therapeutic or toxic activities. The nucleic acid/protein (NAP) conjugates are useful in diagnostic assays and in research candidituding clinical pharmacology, functional genomics, pharmacogenomics, againtient chemicals, environmental safety assessment, chemicals ensorr, nutrient biology, cosmetic research or enzymelogy. These may also be used in in vitro screening techniques and in assays with target molecules. The former is an enzyme attachment site (EAS) DNA used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCAGGCCGGGCGACCAAGGTCGCC
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100.0%; Pred. No. 8.3e-30;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 50B; 127pp; English
                                                                                      14-DEC-2000; 2000US-0256163P.
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Local Similarity 100.
Les 145; Conservative
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                                                                                                                                                                                                                                                                  Liu Y;
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds. Adeno-associated virus (AAV) vector plasmid #1.

BP.

AAD37254 standard; DNA; 955

RESULT 14

(first entry)

21-AUG-2002

AAD37254;

Homo sapiens Unidentified

27-APR-2001; 2001WO-US013677. 28-APR-2000; 2000US-0200777P

WO200183695-A2

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence
The present invention relates to an isolated nuclectide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, Hi and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) and secker muscular vector plasmid containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence
                                                                                                                                                                                                                                                                                                  New dystrophin minigene for treating Duchenne or Becker muscular
dystrophy comprises an N-terminal domain or modified N-terminal domain,
rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 145; DB 6; Length 955; 100.0%; Pred. No. 9.1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 57; 71pp; English.
                                                                                                             27-APR-2001; 2001WO-US013677.
                                                                                                                                                   28-APR-2000; 2000US-0200777P
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                                                                                                                                                                                       (XIAO/) XIAO X.
                                     WO200183695-A2
                                                                           08-NOV-2001
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin

WPI; 2002-049342/06.

(XIAO/) XIAO X.

Kiao X;

Example 1; Page 57; 71pp; English.

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955 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCATGAGGCCGGGCGACCAAAGGTCGCC
                                                                                                                                                                 1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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100.0%; Score 145; DB 6; Length 955; 100.0%; Pred. No. 9.1e-30; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                    121 GCCAACTCCATCACTAGGGGTTCCT 145
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GCCAACTCCATCACTAGGGGTTCCT 145

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GCCAACTCCATCACTAGGGGTTCCT

AAD37254 standard; DNA; 955

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Homo sapiens. Unidentified. Chimeric.

Adeno-associated virus (AAV) vector plasmid #1.

(first entry)

21-AUG-2002

AAD37254;

836

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Sequence 955 BP; 177 A; 307 C; 296 G; 175 T; 0 U; 0 Other;

896 120 us-10-620-039-1.rge

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April 1, 2004, 14:05:53 ; Search time 1825.39 Seconds (without alignments) 3442.959 Million cell updates/sec
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145
1 TIGGCCACTCCCTCTTGCG.......CTCCATCACTAGGGGTTCCT 145
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Description		01 Sequence	1624 Adeno-a	Adeno-as	AR034135 Sequence	ednence	AX106702 Sequence	Adeno-a	Sequence	adeno-as	AX135805 Sequence	Sequenc	Sequence	Method of	Adeno-as	, sequence	AD028767 Semience	162303 Semience	BD242774 Adeno-ass	BD242775 Adeno-ass	AF028704 Adeno-ass	AR235457 Sequence	AR235457 Sequence	AKZ35461 Sequence	AK235401 Sequence AR235454 Semence	AR235454 Sequence	AR235459 Sequence	AR235459 Sequence	AR235462 Sequence	AR235462 Sequence	ARZ35463 Sequence	ARZ35463 Sequence	20235464 Sequence	AR235464 Sequence	AR235460 Seguence	AR235456 Sequence	AR235456 Sequence	AR235455 Sequence	Sequenc	Seduenc	AR222044 Sequence			linear PAT 07-MAR-1997						and Vigne, E.	To a second	
QI	-	-4	rrı Tri	Ĕ,	AK034135	30000TT	AX106702	BD218219	AX703496	AA2LEFT	AX135805	AX286292	AX753252	BD094552	AAZCG	AA664460 ABOA3303	AD028767	T62303	BD242774	BD242775	AF028704	AR235457	AR235457	AK235461 30035461	AR235454	AR235454	AR235459	AR235459	AR235462	AR235462	AK235463	AK235463 ab235464	A. C.	AR235464	AR235460	AR235456	AR235456	AR235455	AK235455	AK655458 20026450	AR222044	ALIGNMENTS		145 bp DNA	nt W09523867.					Latta, M., Perricaudet, M. and		4 08-SEP-1995:
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Ouery Match		45 100.	45 100.	45 100.	. TOO.	100.	100	45 100.	45	45 100.	45 100.	45 100.	45 100.	45 100.	100.		100.	45 100.	45 100.	45 100.	45 100.	45 100.	45 100.	100.	45 100.	45 100.	45 100.	45 100.	45 100.	100.	100.	45 LUU.	. מסלו	45 100.	45 100.	45 100.	45 100.	45 100.	100.	1001	45 100.0			A46401	Sequence 4	6401.1	unidentifie	unidentified	unclassiti(1 (bases)	Denefle, P.,	THERAPEUTIC	Patent: WO
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Adeno-associated virus origin of replication (genome 3' terminus). M10681.1 GI:209626
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Adeno-associated virus 2H
Viruses; ssDNA viruses; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Berns, K.I., Hauswirth, W.W., Fife, K.H. and Lusby, E.
Adeno-associated virus DNA replication
Cold Spring Harb. Symp. Quant. Biol. 43 Pt 2, 781-787 (1979)
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                                                                                                                                           Length 145;
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/organism="Adeno-associated virus 2H"

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/organism="Adeno-associated virus 2H'
/mol type="genomic DNA"
/db_Xref="taxon:10805"
                                                                                                                                        Query Match 100.0%; Score 145; DB 14; Best Local Similarity 100.0%; Pred. No. 1.5e-23; Matches 145; Conservative 0; Mismatches 0;
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Sequence 1 from patent US 5869305.
AR034135
AR034135.1 GI:5949740
                                                 /mol_type="genomic DNA"
/db_xref="taxon:10805"
2 bases upstream of HaeIII site.
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Both [1] and [2] present the opposite strand from the one presented here. The focus of both papers is the method of replication of the virus. [1] notes that the initial tt is present only 30% of the time; it is shortened to tin 50% of the population and missing altogether in 15% of the population. There is further sequence heterogeneity which can be explained by assuming that the terminal 125 bases, which form an imperfect palindrome, are replaced by their inverted complement during replication. [2] found that deletion of the 9 terminal bases on the right and the 113 terminal bases on the left of AAV 2 genome did not stop DNA replication. Further deletion of an 11-base symmetrical sequence (bases 89 to 99) in the right terminal repetition inhibits DNA replication. Substitution of either an 8-base (cagarctgo) or 12-base (caggarctgo) symmetrical sequence unrelated to the original 11-base sequence restores DNA replication. All of this can be explained by assuming that the 125 base palindrome mentioned above
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polymerase during replication.
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Adeno-associated virus 2H
Viruses 98DNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Lusby,E., Fife,K.H. and Berns,K.I.
Nucleotide sequence of the inverted terminal repetition in adeno-associated virus DNA
J. Virol. 34 (2), 402-409 (1980)
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Lefebvre, R.B., Riva, S. and Berns, K.I.
Conformation takes precedence over sequence in adeno-associated
virus DNA replication
MOI. Cell. Biol. 4 (7), 1416-1419 (1984)
85061247
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RHONE POULENC RORER SA (FR)
Other publication AN 1822695 950918
Other publication FR 2116893 950908
Location/Qualifiers

    .145
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Matches 145; Conservative
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AUTHORS TITLE JOURNAL MEDLINE

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Adeno-associated viruses and uses thereof
Patent: WO 0125465-A 7 12-APR-2001;
University of Iowa Research Foundation (US); Engelhardt, John (US); Dongsheng, Duan (US); Ziying, Yan (US)
Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 145; Conservative 0; Mismatches 0;
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ive 0; Mismatches 0;
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           Unclassified.

1 (bases 1 to 165)

Engelhardt,J.F. and Duan,D.
Adeno-associated virus vectors

Patent: US 6436392-A 7 20-AUG-2002;
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    /mol_type="genomic DNA"

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                                                                                                                                                                                                                                                                                               Length 165;
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1 (bases 1 to 165)
SamulbKi,N. and Xiao,X.
Recombinant viral vector system
Patent: US 5478745-A 1 26-DEC-1995;
Location/Qualifiers
                       Camularia. Loudon variante la Gramularia. Loudon variant vector system patent: US 5669305-A 1 09-FEB-1999; Location/Qualifiers

    165
/organism="unknown"
/mol_type="unassigned DNA"

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Sequence 7 from patent US 6436392.
AR223306
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Sequence 1 from patent US 5478745.
116806
116806.1 GI:1251714
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(bases 1 to 2116)

(bases 1 to 2116)

Lusby,E.W. and Berns,K.I.

Mapping of the Strenini of two adeno-associated virus 2 RNAs in the left half of the genome

J. Virol. 41 (2), 518-526 (1982)

82192580

Original source text: adeno-associated virus 2 from human hela cells.
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Repo-associated virus aav rep78 major regulatory protein, mutants
thereof and uses thereof
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Adeno-associated virus 2
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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2116 bp DNA linear adeno-associated virus 2 left half 45% of genome.
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/mol_type="genomic DNA"
/db_xref="taxon:10804"
                                  100.0%; Pred. No. 1.5e-23;
:ive 0; Mismatches 0;
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Sequence 5 from Patent W00132711.
AX135805 GI:14272040
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Adeno-associated virus
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J01902.1 GI:209622
                                  Best Local Similarity 100. Matches 145; Conservative
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28-XAY-2002
20-WAY-1999 JP 2000549752
20-WAY-1999 US 60/086166,25-MAR-1999 US 09/276625 PI
F ENGELHARDT, DONGSHENG DUAN, TUTIN YANG
CI2N15/00, A01K67/027, A61K31/711, A61K48/00, C07K14/47, C12N5/10, C12N15/00,
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    .207
    /organism="synthetic construct"
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    /db.xref="taxon:32650"
    /noTe="synthetic enzyme attachment site sequence"

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Length 165;
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Procaryoric libraries and uses
Patent: WO 02066653-A 58 29-AUG-2002;
Xencor (US)
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Sequence 58 from Patent WO02066653.
AX703496
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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synthetic construct
artificial sequences.
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Asada, K. and Kato, T. and T.
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29-OCT-1999 JP 99P 308839
TAKASHI UENO,HAJIME MATSUMURA,KEIJI TANAKA,TOMOKO IWASAKI, PI
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Adeno-associated virus 2
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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                       1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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1. 4675
/organism="Adeno-associated virus 2"
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100.0%; Pred. No. 9.3e-24;
ive 0; Mismatches 0;
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AX753252 4X53252.1 GI:32166109
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Patent: WO 0132711-A 5 10-MAY-2001;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
Location/Qualifiers
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Pred. No. 9.3e-24;
Mismatches 0; Indels 0
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                                                                                     'organism="Adeno-associated virus
|mol_type="unassigned DNA"
|db_xref="taxon:10804"
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Cycganism="Adeno-associated virus
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llarity 100.0%; Pred. No. 9.3e-24;
Conservative 0; Mismatches 0;
                                                                                                                                                                             'note="unnamed protein product"
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Cytotoxic agents
Patent: WO 0180840-A 1 01-NOV-2001;
BTG INTERNATIONAL LIMITED (GB)
Location/Qualifiers
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Sequence 1 from Patent WO0180840.
AX286292.1 GI:17048540
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tive 0;
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Adeno-associated virus
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Best Local Similarity 100.
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Srivastava, A., Lusby, E.W. and Berns, K.I.
Nucleotide sequence and organization of the adeno-associated virus
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Original source text: Adeno-associated virus 2 DNA from human HeLa
cells:
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PI KEI FUJINADA,KIYOZO ASADA,IKUNOSHIN KATO
PC CIZNIS/861,A61K35/12,A61K35/76,A61K48/00,C12N5/10,C12N7/01 CC
Method of transferring gene
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                                                                                                                                                                                                                                                                                                              TTGGCCACTCCCTCTCTGGCGCTCGCTCGCTCAGGGCCGGGGGACCAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alternative splitting. complete genome; major coat protein.
Adeno-associated virus 2
Adeno-associated virus 2
Viruses; ssplM, viruses; Parvoviridae; Parvovirinae; Dependovirus.

1 (bases 453 to 4675)
Samulski,R.J., Srivastava,A., Berns,K.I. and Muzyczka,N.
Rescue of adeno-associated virus from recombinant plasmids: gene correction within the terminal repeats of AAV
                                                                                                                                                                                                                                                                                           TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGAAAGGTCGCC
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                                                                                 /organism='Adeno-associated virus'.
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100.0%; Score 145; D3 6; Length 46
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 145; Conservative 0; Mismatches 0; Indels
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/note="major coat protein A mRNA (alt.)"
join(321. .1906,2228. .2252)
/note="major coat protein A' (alt.)"

    .4675
forganism="Adeno-associated virus 2"
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    db_xref="taxon:10804"
    .145

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                                                              Location/Qualifiers
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/db_xref="G1:209617"
                                                                                                                             1. .4675
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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J. Virol. 45 (2), 555-564 (1983)
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RTHTMLFGAPATGKTNAIABALAHTVPEPTGVNWTHSNFPFNDCVDKWYLWESKRYTA
KVVESAKALLGGSKYKDQKCKSSAQIDPFPVIVTSYTNMCAVIDGKSTTFEBGQPLQ
DRMFKRELITRRILDHDFGKVTKQEVKDFFRWAKDHVVEVEHEFYVKKGGAKKRPAPSDA
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LIDEQAPLYTVAEKLORDFITBRRRYSKAFBALFFVQFEKGSSFYFHVLVETTGYKS
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TQPELQMAWTNWEQYLSACLNLTERKRLVAQHLTHVSGTQECNKENONPNSDAPVIRS
TXTSAXTMELGVGHLVDKGITSEKQWIDEDQASYISTSRAASKNSTRSQIKAALDNAGKINSL
TXTARDYLVGQQPYBLSISSNRIYKILELNGTVPPQYAASVFLGWATKKFGKRNYIWLFG
PATTGKTNIABALAHTVPFYGCVNWTNENFPPNDCVDKWVIWWEGGNTAKVVESAKA
TLGGSKKYNDQKKSSAQIDFTPVITVSTNTNKCAVIGGNSTTFEHQQPLQDRNFKFEL
TRENDHDFGKXTKQPWCDFFFWAACHVVEVTHEFYVKKGGAKKRPABSDADISBFKKY
TRESVAQPSTSDAEASINYADRLARGHSL"
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MVLGRFLSQIREKLIORIYGETEPTLPNWFAVTKTRNGAGGGKKVUDECYIPRYLLPK
POPELOMANTNEQYLSACLMLTEKKAVAQHITHVSOTGEGNKENUDNENSDAPVIRS
KTSARYMELVGWLONGTITERKAVAQHITHVSOTGEGNKENUNNSDAPVIRS
KTSARYMELVGWLONGTITERKOWIDDDASYISFNAASUSKSOIKAALDDNAGKIMSI
TKTAPDYLVGQOPVEDISSNRIYKILELNGYDPQYAASUSKOKAMATKKFGKRYTTWLFG
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ILGGSKVRVDQKCKSSAQIDPTPVIYTSNTNNCAVIDGNSTTFEHQQDLQDRMFKFEL
TRRLDHDFGKYTKQBVUSPFFWAXCDHVVEVEHRFYVKKGGAKKRPAPSDADISBFKRY
RESVAQPSTSDAAASINYADRYQNKCSRHVGMNAMEPPCRQCERMNONSUICFTHGQX
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KVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVISNTNMCAVIDGNSTTFEHQQPLQ
DRMFKFELTRRLDHDFGKVTKQEVKDFFRWAKDHVVEVEHEFYVKKGGAKKRPAPSDA
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ICFTHGQKDCLECFPVSESQPVSVVKKAYQKLCYIHHIMGKVPDACTACDLVNVDLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCLECFPVSESQPVSVVKKAYQKLCYIHHIMGKVPDACTACDLVNVDLDDCIFEQ"
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/note="major coat protein B mRNA (alt.)"
1907. .2227
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horte="major coat protein A mRNA (alt.)"
join(993. .1906,2228. .2252)
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/note="major coat protein A'' (alt.)"
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/note="3' inverted terminal repeat"
4592. .4634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codon start=1
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0; Gaps
                                    Query Match 100.0%; Score 145; DB 14; Length 4675; Best Local Similarity 100.0%; Pred. No. 9.3e-24; Matches 145; Conservative 0; Mismatches 0; Indels 0;
/note="flop oriented DNA" 5' end of genomic DNA.
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